

**SEARCH REQUEST FORM**

Scientific and Technical Information Center

57382

Requester's Full Name

J. Hines

Examiner # : \_\_\_\_\_

Date: 1/3/02

Art Unit: 1645

Phone Number 305-0487

Serial Number: 091335.581

Mail Box and Bldg/Room Location: CM1 9A71C Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

\*\*\*\*\*

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention:

Peptide for toxic Shock Syndrome

Inventors (please provide full names):

Jason D. Bannan, Kumar Visvanathan

JOHN B. ZABISKIE

Earliest Priority Filing Date:

6/18/99

\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please search the inventor and

Please search SEQ ID NO: 3 and 34

Thanks

Point of Contact:

Mona Smith

Technical Info. Specialist

CM1 12C14 Tel: 308-3278

## STAFF USE ONLY

Type of Search

Vendors and cost where applicable

Searcher: \_\_\_\_\_

NA Sequence (#) \_\_\_\_\_

STN \_\_\_\_\_

AA Sequence (#) \_\_\_\_\_

Dialog \_\_\_\_\_

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=> fil hcaplu

FILE 'HCAPLUS' ENTERED AT 11:26:24 ON 03 JAN 2002

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FILE COVERS 1907 - 3 Jan 2002 VOL 136 ISS 1

FILE LAST UPDATED: 2 Jan 2002 (20020102/ED)

This file contains CAS Registry Numbers for easy and accurate substance identification.

This file supports REGISTRY for direct browsing and searching of all substance data from the REGISTRY file. Enter HELP FIRST for more information.

HCAplus now provides online access to patents and literature covered in CA from 1907 to the present. Bibliographic information and abstracts were added in 2001 for over 3.8 million records from 1907-1966.

CAS roles have been modified effective December 16, 2001. Please check your SDI profiles to see if they need to be revised. For information on CAS roles, enter HELP ROLES at an arrow prompt or use the CAS Roles thesaurus (/RL field) in this file.

=> d stat que

L1 14 SEA FILE=HCAPLUS ("BANNAN J D"/AU OR "BANNAN JASON"/AU OR  
"BANNAN JASON D"/AU OR "BANNAN JASON D"/IN OR "BANNAN JASON  
DAVID"/AU)  
L2 19 SEA FILE=HCAPLUS ("VISVANATHAN K"/AU OR "VISVANATHAN K S"/AU  
OR "VISVANATHAN KANNA V"/AU OR "VISVANATHAN KUMAR"/AU OR  
"VISVANATHAN KUMAR"/IN)  
L3 73 SEA FILE=HCAPLUS ("ZABRISKIE J"/AU OR "ZABRISKIE J B"/AU) OR  
("ZABRISKIE JOHN"/AU OR "ZABRISKIE JOHN B"/AU OR "ZABRISKIE  
JOHN B"/IN)  
L4 2 SEA FILE=HCAPLUS L1 AND L2 AND L3

=> d ibib abs hitrn l4 1-2

L4 ANSWER 1 OF 2 HCAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 2001:76096 HCAPLUS

DOCUMENT NUMBER: 134:250923

TITLE: Inhibition of bacterial superantigens by peptides and  
antibodies

AUTHOR(S): Visvanathan, Kumar; Charles, Alain;

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**Bannan, Jason; Pugach, Pavel; Kashfi, Khosrow; Zabriskie, John B.**  
CORPORATE SOURCE: Laboratory of Clinical Microbiology and Immunology,  
Rockefeller University, New York, NY, 10021, USA  
SOURCE: Infect. Immun. (2001), 69(2), 875-884  
CODEN: INFIBR; ISSN: 0019-9567  
PUBLISHER: American Society for Microbiology  
DOCUMENT TYPE: Journal  
LANGUAGE: English

AB The pyrogenic exotoxins of group A streptococci and staphylococcal enterotoxins are a family of structurally related superantigens with similar biol. activity. Two distinct areas have been identified which have a highly conserved amino acid homol. in all of the toxin families. A no. of peptides were constructed from these regions, some of which were concatenated and polymd. to enhance their immunogenicity in animals. Antibodies prepd. against these polymd. peptides were used to serol. identify the majority of the superantigen toxins, block the biol. activities of the superantigens, and protect an exptl. animal model against shock. In addn. certain peptides were able per se to block up to 90% of the proliferative responses induced by the toxins. The peptide also proved protective in a septic shock model in mice. Binding expts. indicate that the peptide binds tightly to the major histocompatibility complex class II mol., thus preventing binding and hence activation of the superantigen. The selective and rapid binding of the peptide to the major histocompatibility complex class II mol. may lead to a novel therapeutic modality in treatment of superantigen-mediated diseases.

REFERENCE COUNT: 23

REFERENCE(S): (1) Arad, G; Nat Med 2000, V6, P414 HCAPLUS  
(2) Bannan, J; Adv Exp Med Biol 1997, V418, P903 HCAPLUS  
(4) Blank, C; Eur J Immunol 1997, V27(4), P825 HCAPLUS  
(5) Eriksson, A; Microb Pathog 1998, V25, P279 HCAPLUS  
(6) Fridkis-Hareli, M; J Immunol 1998, V160(9), P4386 HCAPLUS

ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 2 OF 2 HCAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 2000:241505 HCAPLUS

DOCUMENT NUMBER: 132:290233

TITLE: Sequences of peptides derived from staphylococcal and streptococcal toxins, and applications thereof in diagnosing and treating toxic shock syndrome and septic shock

INVENTOR(S): **Bannan, Jason D.; Visvanathan, Kumar; Zabriskie, John B.**

PATENT ASSIGNEE(S): Rockefeller University, USA

SOURCE: PCT Int. Appl., 115 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.

KIND DATE

APPLICATION NO. DATE

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WO 2000020598      A1      20000413      WO 1999-US22180  19990924
W:  AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU,
    CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL,
    IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD,
    MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK,
    SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY,
    KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE,
    DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF,
    CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
AU 9960597          A1      20000426      AU 1999-60597      19990924
EP 1127132          A1      20010829      EP 1999-970123     19990924
R:  AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
    IE, SI, LT, LV, FI, RO
PRIORITY APPLN. INFO.:      US 1998-168303  A  19981007
                                US 1999-335581  A  19990618
                                WO 1999-US22180  W  19990924

```

OTHER SOURCE(S):            MARPAT 132:290233

AB This invention relates to amino acid sequences of peptides useful for providing protection against, or reducing the severity of, toxic shock and septic shock resulting from bacterial infections. More particularly, the invention provides peptides derived from consensus sequences of the family of staphylococcal and streptococcal toxins, and may be polymeric and/or carrier-conjugates thereof. The invention also relates to serum antibodies induced by the peptides and/or carrier-conjugates and their use to prevent, treat, or protect against the toxic effects of most, if not all, of the staphylococcal and streptococcal toxins. Antibodies may be induced by administration of a pharmaceutical compn. and/or vaccine contg. a peptide of the invention. The invention also relates to diagnostic assays and kits to detect the presence of staphylococcal and streptococcal toxins, or antibodies thereto.

REFERENCE COUNT:            5

REFERENCE(S):            (1) Bannan, J; WO 9845325 A 1998 HCAPLUS  
                           (2) Bannan, J; INFECTIOUS DISEASE CLINICS OF NORTH  
                                  AMERICA 1999, V13(2), P387 MEDLINE  
                           (3) National Jewish Center For Immunology And  
                                  Respiratory Medicine; WO 9636366 A 1996 HCAPLUS  
                           (4) Schlievert, P; WO 9640930 A 1996 HCAPLUS  
                           (5) Terman, D; WO 9110680 A 1991 HCAPLUS

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 2, 2002, 20:46:42 : Search time 40.75 Seconds  
(without alignments)  
6.627 Million cell updates/sec

Title: US-09-335-581A-34

Perfect score: 71

Sequence: 1 CMYGVTLHEGN 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Issued\_Patents\_AA:\*

- 1: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep:\*
- 2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep:\*
- 3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep:\*
- 4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep:\*
- 5: /cgn2\_6/ptodata/2/1aa/PCRTUS.COMB.pep:\*
- 6: /cgn2\_6/ptodata/2/1aa/backfilea1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	71	100.0	14	4	US-08-896-933-13
2	64	90.1	12	3	US-08-838-413A-3
3	64	90.1	12	3	US-08-838-413A-11
4	64	90.1	14	3	US-08-838-413A-5
5	64	90.1	14	4	US-08-896-933-5
6	64	90.1	36	3	US-08-838-413A-7
7	64	90.1	38	4	US-08-838-413A-8
8	64	90.1	238	4	US-08-896-933-28
9	64	90.1	239	4	US-08-896-933-27
10	62	87.3	12	3	US-08-838-413A-9
11	62	87.3	12	3	US-08-838-413A-13
12	62	87.3	14	4	US-08-896-933-1
13	62	87.3	14	4	US-08-896-933-9
14	62	87.3	23	1	US-08-230-378-5
15	62	87.3	23	2	US-08-696-012-5
16	62	87.3	226	4	US-08-896-933-24
17	62	87.3	232	4	US-08-896-933-23
18	62	87.3	233	1	US-08-446-918A-4
19	62	87.3	257	3	US-08-486-099-112
20	62	87.3	257	3	US-08-486-099-112
21	62	87.3	257	3	US-08-360-107A-122
22	62	87.3	257	3	US-08-360-107A-123
23	62	87.3	257	3	US-08-484-223B-112
24	62	87.3	257	3	US-08-484-223B-113
25	62	87.3	257	3	US-08-919-597-112
26	62	87.3	257	3	US-08-919-597-113
27	62	87.3	257	3	US-08-919-597-113

28	62	87.3	257	3	US-08-475-668A-112	Sequence 112, App
29	62	87.3	257	3	US-08-475-668A-113	Sequence 113, App
30	62	87.3	257	3	US-08-485-551A-112	Sequence 113, App
31	62	87.3	257	3	US-08-485-551A-113	Sequence 113, App
32	62	87.3	257	3	US-08-471-913A-112	Sequence 112, App
33	62	87.3	257	3	US-08-471-913A-113	Sequence 113, App
34	62	87.3	257	4	US-08-485-264A-112	Sequence 112, App
35	62	87.3	257	4	US-08-485-264A-113	Sequence 113, App
36	61	85.9	220	4	US-08-896-933-20	Sequence 20, App
37	60	84.5	12	3	US-08-838-413A-15	Sequence 15, App
38	60	84.5	14	4	US-08-896-933-11	Sequence 11, App
39	60	84.5	221	4	US-08-896-933-29	Sequence 29, App
40	59	83.1	12	3	US-08-838-413A-10	Sequence 10, App
41	59	83.1	13	4	US-08-896-933-3	Sequence 3, App
42	59	83.1	239	4	US-08-896-933-26	Sequence 26, App
43	59	83.1	235	1	US-08-446-918A-2	Sequence 2, App
44	59	83.1	255	2	US-08-580-806-2	Sequence 2, App
45	58	81.7	12	3	US-08-838-413A-12	Sequence 12, App

#### ALIGNMENTS

```
RESULT 1
US-08-896-933-13
Sequence 13, Application US/08896933
Patent No. 6221351
GENERAL INFORMATION:
APPLICANT: Terman, David S.
TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
FILE REFERENCE: 09629/005002
CURRENT APPLICATION NUMBER: US/08/896,933
EARLIER FILING DATE: 1997-07-18
EARLIER APPLICATION NUMBER: 08/252,978
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 13
LENGTH: 14
TYPE: PRT
ORGANISM: Other
FEATURE:
OTHER INFORMATION: Consensus sequences derived from staphylococcus
US-08-896-933-13

Query Match 100.0%; Score 71; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.7e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CMYGVTLHEGN 12
Db 1 CMYGVTLHEGN 12

RESULT 2
US-08-838-413A-3
Sequence 3, Application US/08838413A
Patent No. 6075119
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: PEPTIDES USEFUL FOR
REDUCING SYMPTOMS OF TOXIC SHOCK SYNDROME
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
```

AT 6,122,351  
AT 6,126,945  
10/3/00

ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/838,413A  
FILING DATE: 07-APR-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: MORRY, MARY J.  
REGISTRATION NUMBER: 34,398  
REFERENCE/DOCKET NUMBER: 2016-4010  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)751-6800  
TELEFAX: (212)751-6849  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12  
TYPE: AMINO ACID  
STRANDEDNESS: UNKNOWN  
TOPOLOGY: UNKNOWN  
MOLECULE TYPE: PEPTIDE  
US-08-838-413A-3

Query Match  
Best Local Similarity 90.1%; Score 64; DB 3; Length 12;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGVTLHEGN 12  
| | | | | | | | | | | | | |  
Db 1 CMYGVTEHEGN 12

RESULT 3  
US-08-838-413A-11  
Sequence 11, Application US/08838413A  
Patent No. 6075119  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: PEPTIDES USEFUL FOR  
NUMBER OF INVENTION: REDUCING SYMPTOMS OF TOXIC SHOCK SYNDROME  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/838,413A  
FILING DATE: 07-APR-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: MORRY, MARY J.  
REGISTRATION NUMBER: 34,398

REFERENCE/DOCKET NUMBER: 2016-4010  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)758-4800  
TELEFAX: (212)751-6849  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12  
TYPE: AMINO ACID  
STRANDEDNESS: UNKNOWN  
TOPOLOGY: UNKNOWN  
MOLECULE TYPE: PEPTIDE  
US-08-838-413A-11

Query Match  
Best Local Similarity 90.1%; Score 64; DB 3; Length 12;  
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGVTLHEGN 12  
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Db 1 CMYGVTLHEGN 12

RESULT 4  
US-08-838-413A-5  
Sequence 5, Application US/08838413A  
Patent No. 6075119  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: PEPTIDES USEFUL FOR  
NUMBER OF INVENTION: REDUCING SYMPTOMS OF TOXIC SHOCK SYNDROME  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/838,413A  
FILING DATE: 07-APR-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: MORRY, MARY J.  
REGISTRATION NUMBER: 34,398  
REFERENCE/DOCKET NUMBER: 2016-4010  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)758-4800  
TELEFAX: (212)751-6849  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14  
TYPE: AMINO ACID  
STRANDEDNESS: UNKNOWN  
TOPOLOGY: UNKNOWN  
MOLECULE TYPE: PEPTIDE  
US-08-838-413A-5

Query Match  
Best Local Similarity 90.1%; Score 64; DB 3; Length 14;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGGVTLHEGN 12  
| | | | | | | | | |  
Db 1 CMYGGVTEHEGN 12

## RESULT 5

US-08-896-933-5

Sequence 5, Application US/08896933

Patent No. 6221351

GENERAL INFORMATION:

APPLICANT: Yerman, David S.

TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,

FILE REFERENCE: 09629/005002

CURRENT APPLICATION NUMBER: US/08/896,933

EARLIER FILING DATE: 1997-07-18

EARLIER FILING DATE: 1994-06-02

NUMBER OF SEQ ID NOS: 34

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 5

LENGTH: 14

TYPE: PRT

ORGANISM: Staphylococcus aureas

US-08-896-933-5

Query Match 90.1%; Score 64; DB 4; Length 14;  
Best Local Similarity 83.3%; Pred. No. 7.1e-05;  
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGGVTLHEGN 12  
| | | | | | | | | |  
Db 1 CMYGGVTEHEGN 12

## RESULT 6

US-08-838-413A-7

Sequence 7, Application US/08838413A

Patent No. 6075119

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: PEPTIDES USEFUL FOR

REDUCING SYMPTOMS OF TOXIC SHOCK SYNDROME

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:

ADDRESS: MORGAN & FINNEGAN

STREET: 345 PARK AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/838,413A

FILING DATE: 07-APR-1997

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: MORRY, MARY J.

REGISTRATION NUMBER: 34,398

REFERENCE/DOCKET NUMBER: 2016-4010

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)758-4800

TELEFAX: (212)751-6849

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 36

TYPE: AMINO ACID

STRANDEDNESS: UNKNOWN

TOPOLOGY: UNKNOWN

MOLECULE TYPE: PEPTIDE

US-08-838-413A-7

Query Match 90.1%; Score 64; DB 3; Length 36;  
Best Local Similarity 91.7%; Pred. No. 0.00019;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGGVTLHEGN 12  
| | | | | | | | | |  
Db 1 CMYGGVTEHEGN 12

## RESULT 7

US-08-838-413A-8

Sequence 8, Application US/08838413A

Patent No. 6075119

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: PEPTIDES USEFUL FOR

REDUCING SYMPTOMS OF TOXIC SHOCK SYNDROME

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:

ADDRESS: MORGAN & FINNEGAN

STREET: 345 PARK AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/838,413A

FILING DATE: 07-APR-1997

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: MORRY, MARY J.

REGISTRATION NUMBER: 34,398

REFERENCE/DOCKET NUMBER: 2016-4010

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)758-4800

TELEFAX: (212)751-6849

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 38

TYPE: AMINO ACID

STRANDEDNESS: UNKNOWN

TOPOLOGY: UNKNOWN

MOLECULE TYPE: PEPTIDE

US-08-838-413A-8

Query Match 90.1%; Score 64; DB 3; Length 38;  
Best Local Similarity 91.7%; Pred. No. 0.0002;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGGVTLHEGN 12  
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Db 1 CMYGGVTEHGN 12

RESULT 8

US-08-896-933-28  
; Sequence 28, Application US/08896933  
; Patent No. 6221351

GENERAL INFORMATION:

APPLICANT: Terman, David S.

TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,

FILE REFERENCE: 09629/005002

CURRENT APPLICATION NUMBER: US/08/896,933

EARLIER FILING DATE: 1997-07-18

EARLIER FILING DATE: 1994-06-02

NUMBER OF SEQ ID NOS: 34

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 28

LENGTH: 238

TYPE: PRT

ORGANISM: Staphylococcus aureas

US-08-896-933-28

Query Match

Best Local Similarity 90.1%; Score 64; DB 4; Length 238;

Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CMYGGVTEHGN 12

Db 109 CMYGGITKHEGN 120

RESULT 9

US-08-896-933-27

Sequence 27, Application US/08896933

Patent No. 6221351

GENERAL INFORMATION:

APPLICANT: Terman, David S.

TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,

FILE REFERENCE: 09629/005002

CURRENT APPLICATION NUMBER: US/08/896,933

EARLIER FILING DATE: 1997-07-18

EARLIER FILING DATE: 1994-06-02

NUMBER OF SEQ ID NOS: 34

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 27

LENGTH: 239

TYPE: PRT

ORGANISM: Staphylococcus aureas

US-08-896-933-27

Query Match 90.1%; Score 64; DB 4; Length 239;

Best Local Similarity 83.3%; Pred. No. 0.0014;

Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CMYGGVTEHGN 12

Db 110 CMYGGITKHEGN 121

RESULT 10

US-08-838-413A-9

Sequence 9, Application US/08838413A

Patent No. 6075119

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION:

PEPTIDES USEFUL FOR

TITLE OF INVENTION: REDUCING SYMPTOMS OF TOXIC SHOCK SYNDROME

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN

STREET: 345 PARK AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/838,413A

FILING DATE: 07-APR-1997

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: MORRY, MARY J.

REGISTRATION NUMBER: 34,398

REFERENCE/DOCKET NUMBER: 2016-4010

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)758-4800

TELEFAX: (212)751-6849

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 12

TYPE: AMINO ACID

STRANDEDNESS: UNKNOWN

TOPOLOGY: UNKNOWN

MOLECULE TYPE: PEPTIDE

US-08-838-413A-9

Query Match

Best Local Similarity 87.3%; Score 62; DB 3; Length 12;

Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CMYGGVTEHGN 12

Db 1 CMYGGVTEHGN 12

RESULT 11

US-08-838-413A-13

Sequence 13, Application US/08838413A

Patent No. 6075119

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: PEPTIDES USEFUL FOR

REDUCING SYMPTOMS OF TOXIC SHOCK SYNDROME

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN

STREET: 345 PARK AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/838,413A

FILING DATE: 07-APR-1997



CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: MORRY, MARY J.  
REGISTRATION NUMBER: 34,398  
REFERENCE/DOCKET NUMBER: 2016-4010  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)758-4800  
TELEFAX: (212)751-6849  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12  
TYPE: AMINO ACID  
STRANDEDNESS: UNKNOWN  
TOPOLOGY: UNKNOWN  
MOLECULE TYPE: PEPTIDE  
US-08-838-413A-13

Query Match 87.3%; Score 62; DB 3; Length 12;  
Best Local Similarity 83.3%; Pred. No. 0.00013;  
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGVTLHEGN 12  
Db 1 CMYGVTLHDNN 12

RESULT 12  
US-08-896-933-1  
Sequence 1, Application US/08896933  
Patent No. 6221351  
GENERAL INFORMATION:  
APPLICANT: Terman, David S.  
TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,  
FILE REFERENCE: 09629/005002  
CURRENT APPLICATION NUMBER: US/08/896,933  
CURRENT FILING DATE: 1997-07-18  
EARLIER APPLICATION NUMBER: 08/252,978  
EARLIER FILING DATE: 1994-06-02  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 1  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Staphylococcus aureus  
US-08-896-933-1

Query Match 87.3%; Score 62; DB 4; Length 14;  
Best Local Similarity 83.3%; Pred. No. 0.00015;  
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGVTLHEGN 12  
Db 1 CMYGVTLHDNN 12

RESULT 13  
US-08-896-933-9  
Sequence 9, Application US/08896933  
Patent No. 6221351  
GENERAL INFORMATION:  
APPLICANT: Terman, David S.  
TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,  
FILE REFERENCE: 09629/005002  
CURRENT APPLICATION NUMBER: US/08/896,933  
CURRENT FILING DATE: 1997-07-18

EARLIER APPLICATION NUMBER: 08/252,978  
EARLIER FILING DATE: 1994-06-02  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 9  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Staphylococcus aureus  
US-08-896-933-9

Query Match 87.3%; Score 62; DB 4; Length 14;  
Best Local Similarity 83.3%; Pred. No. 0.00015;  
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGVTLHEGN 12  
Db 1 CMYGVTLHDNN 12

RESULT 14  
US-08-220-378-5  
Sequence 5, Application US/08220378  
Patent No. 5545716  
GENERAL INFORMATION:  
APPLICANT: Johnson, Howard M.  
APPLICANT: Pontzer, Carol H.  
APPLICANT: Griggs, Nathan D.  
TITLE OF INVENTION: Superantigen Agonist and Antagonist  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Saliwanchik & Saliwanchik  
STREET: 2421 N.W. 1st Street, Suite A-1  
CITY: Gainesville  
STATE: FL  
COUNTRY: USA  
ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/220,378  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/941,497  
FILING DATE: 08-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Saliwanchik, David R.  
REGISTRATION NUMBER: 31,794  
REFERENCE/DOCKET NUMBER: UFI26.C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 904-375-8100  
TELEFAX: 904-372-5800  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 23 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-220-378-5

Query Match 87.3%; Score 62; DB 1; Length 23;  
Best Local Similarity 83.3%; Pred. No. 0.00026;  
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGVTLHEGN 12  
Db 1 CMYGVTLHDNN 12

Db 5 CMYGVTLHDNN 16

RESULT 15

US-08-696-012-5

; Sequence 5, Application US/08696012

; Patent No. 5859207

; GENERAL INFORMATION:

; APPLICANT: Johnson, Howard M.

; APPLICANT: Pontzer, Carol H.

; APPLICANT: Griggs, Nathan D.

; TITLE OF INVENTION: Superantigen Agonist and Antagonist

; TITLE OF INVENTION: Peptides

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Saliwanchik & Saliwanchik

; STREET: 2421 N.W. 41st Street, Suite A-1

; CITY: Gainesville

; STATE: FL

; COUNTRY: USA

; ZIP: 32606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC Compatible

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/696,012

; FILING DATE: 12-AUG-1996

; CLASSIFICATION: 530

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: 08/220,378

; FILING DATE: 29-MAR-1994

; APPLICATION NUMBER: US 07/941,497

; FILING DATE: 08-SEP-1992

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Saliwanchik, David R.

; REGISTRATION NUMBER: 31,794

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 904-375-8100

; TELEFAX: 904-372-5800

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 23 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; US-08-696-012-5

Query Match 87.3%; Score 62; DB 2; Length 23;

Best Local Similarity 83.3%; Pred. No. 0.00026;

Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CMYGVTLHDNN 12

Db 5 CMYGVTLHDNN 16

Search completed: January 2, 2002, 20:46:42  
Job time: 11488 sec

35

Although the foregoing invention has been described in detail for purposes of clarity of understanding, certain modifications may be practiced within the scope of the appended claims. While the above findings apply to an experimental animal model, it should be recognized that the tumor used herein is an excellent model of human cancer. Therapeutic success in the canine model with PACC system (described in a series of patent applications, the latest of which is identified as Ser. No. 331,095), the forerunner of the present invention, was transferred to humans in which objective tumor regressions were obtained in four of the first five consecutive patients treated. Thus, the data given herein for rabbits with carcinoma is expected to be predictive of success when the compositions are applied to humans with spontaneous tumors as well.

In the method of treating cancer in a patient utilizing a single step of administering Staphylococcal enterotoxins or enterotoxin fragments, a tumoricidally effective amount of the enterotoxin or enterotoxin fragment is between 0.5  $\mu$ g (enterotoxin) per kg (body weight) and 1.50  $\mu$ g (enterotoxin) per kg (body weight). This tumoricidally effective amount applies to the enterotoxins which are chemically derivatized.

We claim:

1. A method of treating a subject having a tumor comprising administering to the subject a tumoricidally effective amount of a toxin selected from the group consisting of a staphylococcal enterotoxin and a streptococcal pyrogenic exotoxin.
2. The method of claim 1, wherein the toxin is a staphylococcal enterotoxin.
3. The method of claim 2 wherein the staphylococcal enterotoxin is selected from the group consisting of enterotoxin A, B, C, D, E, and F.
4. The method of claim 2 wherein the staphylococcal enterotoxin is a biologically active fragment of an enterotoxin.
5. The method of claim 2 wherein the staphylococcal enterotoxin has been chemically derivatized to minimize toxicity while retaining tumoricidal activity.

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6. The method of claim 1 wherein the toxin is administered by intravenous inoculation.

7. The method of claim 1 wherein the tumor is a carcinoma.

8. A method of treating a patient having a tumor comprising administering to the patient a tumoricidally effective amount of a toxin selected from the group consisting of a staphylococcal enterotoxin and a streptococcal pyrogenic exotoxin.

9. The method of claim 8 wherein the toxin is a staphylococcal enterotoxin.

10. The method of claim 9 wherein the staphylococcal enterotoxin is selected from the group consisting of enterotoxin A, B, C, D, E, and F.

11. The method of claim 10 wherein the staphylococcal enterotoxin is enterotoxin B.

12. The method of claim 8 wherein the tumor is a carcinoma.

13. The method of claim 9 wherein the staphylococcal enterotoxin is a biologically active fragment of an enterotoxin.

14. The method of claim 9 wherein the staphylococcal enterotoxin has been chemically derivatized to minimize toxicity while retaining tumoricidal activity.

15. The method of claim 9 wherein the chemical derivatization is carboxymethylation.

16. The method of claim 15 wherein the carboxymethylated toxin comprises carboxymethylated enterotoxin B.

17. The method of claim 11 wherein the enterotoxin B has been purified to remove alpha hemolysin.

18. The method of claim 11 wherein the enterotoxin B contains no more than 0.1 microgram endotoxin per milligram enterotoxin B.

19. The method of claim 8 wherein the toxin is administered by intravenous inoculation.

\* \* \* \* \*

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```

225                               230                               235                               240
Arg Ala Lys Leu Asp Lys
      245

<210> SEQ ID NO 34
<211> LENGTH: 27
<212> TYPE: PRT
<213> ORGANISM: Staphylococcal

<400> SEQUENCE: 34

Ser Glu Lys Ser Glu Glu Ile Asn Glu Lys Asp Leu Arg Lys Lys Ser
 1          5          10          15

Glu Leu Gln Gly Thr Ala Leu Gly Asn Leu Lys
      20          25

```

25. The method of claim 23, wherein the activated immunocytes are expanded by in vitro culture prior to their administration.

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26. The method of claim 25, wherein the in vitro culture includes interleukin 2.

27. The method of claim 15 or 16, wherein the superantigen is expressed on the surface of the transfected cells.

28. The method of claim 15 or 16, wherein the transfected cells expresses MHC class II molecules.

29. A method for increasing antitumor immunity against a tumor in a mammal, comprising contacting tumor cells that are transfected with nucleic acid encoding a superantigen or biologically active polypeptide of a superantigen with the immune system of said mammal,

wherein expression of the superantigen or polypeptide by the transfected cells induces T cell proliferation and increases said antitumor immunity.

30. A method for increasing antitumor immunity against a tumor in a mammal, comprising contacting accessory cells, immunocytes or fibroblasts that are transfected with nucleic acid encoding a superantigen or biologically active polypeptide of a superantigen with the immune system of said mammal,

wherein expression of the superantigen or polypeptide by the transfected cells induces T cell proliferation and increases said antitumor immunity.

31. The method of claim 29 or 30, wherein the mammal is a human.

32. The method of claim 29 or 30, wherein the superantigen is selected from the group consisting of a Staphylococcal enterotoxin, a Streptococcal pyrogenic exotoxin, toxic shock syndrome toxin, a mycoplasma antigen, a mycobacteria antigen, a minor lymphocyte stimulating antigen, a heat shock protein, a stress peptide, and a derivative thereof.

33. The method of claim 29 or 30, wherein the tumor cells, accessory cells, immunocytes or fibroblasts are transfected in vivo.

34. The method of claim 29 or 30, wherein the tumor cells, accessory cells, immunocytes or fibroblasts are transfected in vitro.

35. The method of claim 34, wherein the transfected cells are tumor cells, and the contacting comprises administering the transfected tumor cells to the mammal.

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36. The method of claim 29 or 30, wherein the contacting comprises administering the transfected cells to the mammal.

37. The method of claim 29 or 30, wherein the contacting comprises:

(i) incubating the transfected cells ex vivo with an immunocyte population to tumoricidally activate the population, and

(ii) administering the activated population to the mammal.

38. The method of claim 37, wherein the immunocyte population being activated comprises T cells.

39. The method of claim 37, wherein the activated immunocytes are expanded by in vitro culture prior to their administration.

40. The method of claim 39, wherein the in vitro culture includes interleukin 2.

41. The method of claim 29 or 30, wherein the superantigen is expressed on the surface of the transfected cells.

42. The method of claim 29 or 30, wherein the transfected cells express MHC class II molecules.

43. A method for treating cancer in a tumor-bearing host, comprising administering a nucleic acid encoding a superantigen to said tumor in vivo to transfect tumor cells, wherein expression of said superantigen induces a tumoricidal immune response, thereby treating said cancer.

44. A method of killing tumor cells in a mammal, comprising administering a nucleic acid encoding a superantigen or biologically active polypeptide of a superantigen to said tumor in vivo to transfect tumor cells, wherein expression of the superantigen or polypeptide produces a tumoricidal immune response resulting in the killing of said tumor cells.

45. A method for increasing antitumor immunity against a tumor in a tumor-bearing mammal, comprising administering a nucleic acid encoding a superantigen or biologically active polypeptide of a superantigen to said tumor in vivo to transfect tumor cells, wherein expression of the superantigen or polypeptide induces T cell proliferation and increases said antitumor immunity.

46. The method of any of claims 43-45 wherein said mammal or host is a human.

\* \* \* \* \*

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[illegible]

consensus amino acid sequence derived from two conserved regions (regions 1 and 2) of *Staphylococcus aureus* enterotoxins and streptococcal pyrogenic toxins. Consensus region 1a (a preferred consensus region 1) has the sequence X25-X26-Y-G-G-X11-T-X2-X3-X4-X5-N (AAV97863) and consensus region 2a (a preferred consensus region 2) has the sequence K-X6-X7-X8-X9-X10-X11-X12-X13-D-X14-X15-X16-R-X17-X18-X27-X19-X20-X21-X22-X23-X24-Y (AAV97864), where: X1, X8, X13 and X24 are each independently selected from L, I and V; X2, X4, X5, X6, X7, X9, X10, X11, X12, X14, X15, X16, X17, X18, X19, X20, X21, X22 and X23 are each independently selected from the group consisting of any amino acid; X3, X5 and X26 are each independently selected from the group consisting of any amino acid and of no amino acid; X27 is either L or Y.

The invention also relates to serum antibodies induced by the peptides which provide protection against, or reduce the severity of toxic shock and septic shock caused by the staphylococcal and streptococcal pyrogenic toxins. The pyrogenic exotoxins of Group A streptococci and the enterotoxins of *Staphylococcus aureus* (which are also pyrogenic exotoxins) constitute a family of structurally related toxins which share similar biological activities. They stimulate CD4<sup>+</sup>, CD8<sup>+</sup> and gamma-delta<sup>+</sup> T-cells by binding the beta-chain variable region (V-beta) elements on the lateral face of the T-cell receptor (TCR) while simultaneously binding the lateral face of the class II major histocompatibility complex (MHC) of antigen presenting cells. This causes aberrant proliferation of T-cells, which stimulates other components of the immune system, causing injury to the host. The peptides are used to prevent, treat or protect against toxic shock and septic shock resulting from bacterial infections in mammals, particularly humans. The peptides are used for inducing serum antibodies that bind at least one staphylococcal enterotoxin or streptococcal exotoxin and both the peptides and antibodies can be used in diagnostic assays to aid in the diagnosis of disease related to the presence of bacterial toxins. Nucleic acids encoding a peptide of the invention can be used for the production of the peptides for diagnostic reagents, as vaccines and for therapies for pyrogenic exotoxin related diseases. Vectors expressing high levels of the peptides can be used in immunotherapy and immunophylaxis when expressed in humans. The antibodies are used for passive immunisation therapy to prevent or increase resistance to toxic shock syndrome or septic shock and to ameliorate the effects of conditions associated with the presence of staphylococcal or streptococcal pyrogenic toxins. The amino acid sequences of the peptides are sufficiently common that they can be used for eliciting antibodies which are cross-reactive with toxins derived from various bacteria. Sequences AAV97838-978343 represent the synthetic peptides based on consensus consensus regions 1 and 2 of *Staphylococcus aureus* and Group A streptococcal pyrogenic toxins. These peptides can be administered to a mammal to raise serum antibodies for protection against or amelioration of toxic or septic shock.

Sequence 12 AA:

Query Match 100.0%; Score 72; DB 21; Length 12;  
Best Local Similarity 100.0%; Pred. No. 3.5e-06;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 1 CMYGGVTEHEGN 12  
| | | | | | | | | | | | | |  
Db 1 cmgygvtehegn 12

RESULT 3  
AAV72176  
XX AAV72176 standard; peptide: 12 AA.  
XX  
XX AAV72176;  
DT 24-APR-2001 (first entry)  
XX  
XX Peptide #6343, derived from streptococcal and staphylococcal toxins.  
TM Mononuclear cell; blastogenesis; inhibitor; HIV; replication; therapy;  
staphylococcal enterotoxin; human immunodeficiency virus; T cell;

KM streptococcal pyrogenic exotoxin; autoimmune disease; immunisation.  
 XX Streptococcus sp.  
 OS Staphylococcus sp.  
 XX WO200078790-A2.  
 XX  
 PD 28-DEC-2000.  
 XX  
 PF 16-JUN-2000; 2000WO-US16680.  
 XX  
 PR 18-JUN-1999; 99US-0336627.  
 XX  
 PA (UYRO ) UNIV ROCKEFELLER.  
 XX  
 PI Visvanathan K, Zabriskie JB;  
 DR WPI: 2001-080820/09.  
 XX  
 PT Providing protection against, and reducing the severity of, human  
 PT immunodeficiency virus infections and associated deleterious effects,  
 PT using peptides from homologous sequences of staphylococcal and  
 PT streptococcal toxins  
 XX  
 PS Claim 5; Page 38; 76pp; English.  
 XX  
 CC The present sequence is peptide #6343, derived from region 1 of  
 CC the homologous sequences of staphylococcal enterotoxin and  
 CC streptococcal pyrogenic exotoxin.  
 CC The peptide, nucleic acid encoding the peptide and antibody (Ab) produced  
 CC against the peptide are useful for inhibiting blastogenesis of  
 CC mononuclear cells (eg. T cells) in the presence of human immunodeficiency  
 CC virus (HIV), inhibiting HIV replication and protecting a mammal against  
 CC the deleterious effects of HIV. The peptide is also used to ameliorate  
 CC the effects of autoimmune diseases associated with the presence of HIV.  
 CC The Ab is used for passively immunising a mammal against the deleterious  
 CC effects of HIV.  
 XX  
 SQ Sequence 12 AA:  
 Query Match 100.0%; Score 72; DB 22; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-06;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 CMYGVTEHEGN 12  
 Db 1 cmgygvtehegn 12  
 RESULT 4  
 AAW72424  
 ID AAW72424 standard; peptide: 14 AA.  
 XX  
 AC AAW72424;  
 XX  
 DT 22-DEC-1998 (first entry)  
 XX  
 DE Peptide #3 for reducing symptoms of toxic shock syndrome.  
 XX  
 KM Toxic shock syndrome; immunogenic response; bacterial infection;  
 KM staphylococcal enterotoxin; streptococcal pyrogenic toxin; antibody;  
 KM autoimmune disease.  
 XX  
 OS Synthetic.  
 OS Staphylococcus sp.  
 OS Streptococcus sp.  
 XX  
 PN WO9845325-A1.  
 XX  
 PD 15-OCT-1998.  
 XX  
 PF 01-APR-1998; 98WO-US06663.

XX  
 PR 07-APR-1997; 97US-0838413.  
 XX  
 PA (UYRO ) UNIV ROCKEFELLER.  
 XX  
 PI Bannan JD, Zabriskie JB;  
 DR WPI: 1998-568335/48.  
 XX  
 PT New peptides that generate antibodies against staphylococcal and  
 PT streptococcal toxins - used to diagnose, treat or prevent toxic  
 PT shock and autoimmune diseases  
 XX  
 PS Claim 4; Page 53; 69pp; English.  
 XX  
 CC The present invention describes peptides having consensus sequences #1  
 CC or #2, optionally as part of a larger molecule of size at least 6-8 kD.  
 CC Where consensus sequence #1 and #2 are: X25X26YGXITX23X4X5N #1,  
 CC KX6X78X9X10X11X12X13DX14X15X16RX17X18X27X19X20X21X22X23X24Y #2, where  
 CC X1, X8, X13 and X24 = L, I or V; X3, X25 and X26 = any amino acid (aa)  
 CC or are absent; X27 = L or Y; all other X may be any aa. The peptides  
 CC can be used to generate serum antibodies (Ab) that bind at least one  
 CC staphylococcal enterotoxin (SE) or streptococcal endotoxin (SPE). Ab  
 CC are used: (i) for diagnostic detection of SPEA or SEA, SEB and SED, in  
 CC usual immunoassays; (ii) to inhibit blastogenesis of human mononuclear  
 CC cells in presence of these toxins (i.e. to protect against or alleviate  
 CC toxic shock or autoimmune disease associated with bacterial infections);  
 CC and (iii) for passive immunisation against effects of the toxins. The  
 CC peptides generate Ab that are cross-reactive with toxins from a variety  
 CC of bacteria. The present sequence represents a specifically claimed  
 CC example of a peptide of the present invention.  
 XX  
 SQ Sequence 14 AA:  
 Query Match 100.0%; Score 72; DB 19; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-06;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 CMYGVTEHEGN 12  
 Db 1 cmgygvtehegn 12  
 RESULT 5  
 AAY97840  
 ID AAY97840 standard; peptide: 14 AA.  
 XX  
 AC AAY97840;  
 XX  
 DT 29-AUG-2000 (first entry)  
 XX  
 DE Staphylococcal/streptococcal pyrogenic toxin-derived peptide, 6344.  
 XX  
 KM Pyrogenic exotoxin; enterotoxin; streptococcal infection;  
 KM staphylococcal infection; septic shock; toxic shock; vaccine;  
 KM antibody.  
 XX  
 OS Synthetic.  
 OS Staphylococcus aureus.  
 OS Streptococcus sp. 'Group A'.  
 XX  
 PN WO200020598-A1.  
 XX  
 PD 13-APR-2000.  
 XX  
 PF 24-SEP-1999; 99WO-US22180.  
 XX  
 PR 07-OCT-1998; 98US-0168303.  
 PR 18-JUN-1999; 99US-0335581.  
 XX  
 PA (UYRO ) UNIV ROCKEFELLER.  
 XX

PI Bannan JD, Visvanathan K, Zabriskie JB;  
XX  
DR WPI: 2000-303782/26.

PT Peptides useful for preventing and reducing the symptoms of toxic shock  
PT syndrome and septic shock from staphylococcal and streptococcal  
PT infections -

Claim 4; Page 88; 115pp; English.

CC The invention relates to novel peptides (AAV97838-1-Y97843) comprising a  
CC consensus amino acid sequence derived from two conserved regions  
CC (regions 1 and 2) of *Staphylococcus aureus* enterotoxins and  
CC streptococcal pyrogenic toxins. Consensus region 1a, a preferred  
CC consensus region 1) has the sequence X25-X26-Y-G-G-X1-T-X2-X3-X4-X5-N  
CC (AAV97863) and consensus region 2a (a preferred consensus region 2) has  
CC the sequence K-X6-X7-X8-  
CC X9-Y10-X11-X12-X13-D-X14-X15-X16-R-X17-X18-X27-X19-X20-X21-X22-X23-X24-Y  
CC (AAV97864), where: X13, X8, X15 and X24 are each independently selected  
CC from L, I and V; X2, X4, X5, X6, X7, X9, X10, X11, X12, X14, X15, X16,  
CC X17, X18, X19, X20, X21, X22 and X23 are each independently selected from  
CC the group consisting of any amino acid;  
CC X3, X4 and X26 are each independently selected from the group consisting  
CC of any amino acid and of no amino acid;  
CC X1, X2, X5, X7, X9, X10, X11, X12, X13, X14, X15, X16, X17, X18, X19, X20, X21, X22, X23, X24, X25, X27, X28, X29, X30, X31, X32, X33, X34, X35, X36, X37, X38, X39, X40, X41, X42, X43, X44, X45, X46, X47, X48, X49, X50, X51, X52, X53, X54, X55, X56, X57, X58, X59, X60, X61, X62, X63, X64, X65, X66, X67, X68, X69, X70, X71, X72, X73, X74, X75, X76, X77, X78, X79, X80, X81, X82, X83, X84, X85, X86, X87, X88, X89, X90, X91, X92, X93, X94, X95, X96, X97, X98, X99, X100, X101, X102, X103, X104, X105, X106, X107, X108, X109, X110, X111, X112, X113, X114, X115, X116, X117, X118, X119, X120, X121, X122, X123, X124, X125, X126, X127, X128, X129, X130, X131, X132, X133, X134, X135, X136, X137, X138, X139, X140, X141, X142, X143, X144, X145, X146, X147, X148, X149, X150, X151, X152, X153, X154, X155, X156, X157, X158, X159, X160, X161, X162, X163, X164, X165, X166, X167, X168, X169, X170, X171, X172, X173, X174, X175, X176, X177, X178, X179, X180, X181, X182, X183, X184, X185, X186, X187, X188, X189, X190, X191, X192, X193, X194, X195, X196, X197, X198, X199, X200, X201, X202, X203, X204, X205, X206, X207, X208, X209, X210, X211, X212, X213, X214, X215, X216, X217, X218, X219, X220, X221, X222, X223, X224, X225, X226, X227, X228, X229, X230, X231, X232, X233, X234, X235, X236, X237, X238, X239, X240, X241, X242, X243, X244, X245, X246, X247, X248, X249, X250, X251, X252, X253, X254, X255, X256, X257, X258, X259, X260, X261, X262, X263, X264, X265, X266, X267, X268, X269, X270, X271, X272, X273, X274, X275, X276, X277, X278, X279, X280, X281, X282, X283, X284, X285, X286, X287, X288, X289, X290, X291, X292, X293, X294, X295, X296, X297, X298, X299, X300, X301, X302, X303, X304, X305, X306, X307, X308, X309, X310, X311, X312, X313, X314, X315, X316, X317, X318, X319, X320, X321, X322, X323, X324, X325, X326, X327, X328, X329, X330, X331, X332, X333, X334, X335, X336, X337, X338, X339, X340, X341, X342, X343, X344, X345, X346, X347, X348, X349, X350, X351, X352, X353, X354, X355, X356, X357, X358, X359, X360, X361, X362, X363, X364, X365, X366, X367, X368, X369, X370, X371, X372, X373, X374, X375, X376, X377, X378, X379, X380, X381, X382, X383, X384, X385, X386, X387, X388, X389, X390, X391, X392, X393, X394, X395, X396, X397, X398, X399, X400, X401, X402, X403, X404, X405, X406, X407, X408, X409, X410, X411, X412, X413, X414, X415, X416, X417, X418, X419, X420, X421, X422, X423, X424, X425, X426, X427, X428, X429, X430, X431, X432, X433, X434, X435, X436, X437, X438, X439, X440, X441, X442, X443, X444, X445, X446, X447, X448, X449, X450, X451, X452, X453, X454, X455, X456, X457, X458, X459, X460, X461, X462, X463, X464, X465, X466, X467, X468, X469, X470, X471, X472, X473, X474, X475, X476, X477, X478, X479, X480, X481, X482, X483, X484, X485, X486, X487, X488, X489, X490, X491, X492, X493, X494, X495, X496, X497, X498, X499, X500, X501, X502, X503, X504, X505, X506, X507, X508, X509, X510, X511, X512, X513, X514, X515, X516, X517, X518, X519, X520, X521, X522, X523, X524, X525, X526, X527, X528, X529, X530, X531, X532, X533, X534, X535, X536, X537, X538, X539, X540, X541, X542, X543, X544, X545, X546, X547, X548, X549, X550, X551, X552, X553, X554, X555, X556, X557, X558, X559, X560, X561, X562, X563, X564, X565, X566, X567, X568, X569, X570, X571, X572, X573, X574, X575, X576, X577, X578, X579, X580, X581, X582, X583, X584, X585, X586, X587, X588, X589, X590, X591, X592, X593, X594, X595, X596, X597, X598, X599, X600, X601, X602, X603, X604, X605, X606, X607, X608, X609, X610, X611, X612, X613, X614, X615, X616, X617, X618, X619, X620, X621, X622, X623, X624, X625, X626, X627, X628, X629, X630, X631, X632, X633, X634, X635, X636, X637, X638, X639, X640, X641, X642, X643, X644, X645, X646, X647, X648, X649, X650, X651, X652, X653, X654, X655, X656, X657, X658, X659, X660, X661, X662, X663, X664, X665, X666, X667, X668, X669, X670, X671, X672, X673, X674, X675, X676, X677, X678, X679, X680, X681, X682, X683, X684, X685, X686, X687, X688, X689, X690, X691, X692, X693, X694, X695, X696, X697, X698, X699, X700, X701, X702, X703, X704, X705, X706, X707, X708, X709, X710, X711, X712, X713, X714, X715, X716, X717, X718, X719, X720, X721, X722, X723, X724, X725, X726, X727, X728, X729, X730, X731, X732, X733, X734, X735, X736, X737, X738, X739, X740, X741, X742, X743, X744, X745, X746, X747, X748, X749, X750, X751, X752, X753, X754, X755, X756, X757, X758, X759, X760, X761, X762, X763, X764, X765, X766, X7

The invention also relates to serum antibodies induced by the peptides which provide protection against, or reduce the severity of toxic shock and septic shock caused by the staphylococcal and streptococcal pyrogenic toxins. The pyrogenic exotoxins of Group A streptococci and the enterotoxins of *Staphylococcus aureus* (which are also pyrogenic exotoxins) constitute a family of structurally related toxins which share similar biological activities. They stimulate CD4+, CD8+ and gamma-delta+ T-cells by binding of the beta-chain variable region (V-beta) elements on the lateral face of the T-cell receptor (TCR) while simultaneously binding the lateral face of the class II major histocompatibility complex (MHC) of antigen presenting cells. This causes aberrant proliferation of T-cells, which stimulates other components of the immune system, causing injury to the host. The peptides are used to prevent, treat or protect against toxic shock and septic shock resulting from bacterial infections in mammals, particularly humans. The peptides are used for inducing serum antibodies that bind at least one staphylococcal enterotoxin or streptococcal exotoxin and both the peptides and antibodies can be used in diagnostic assays to aid in the diagnosis of disease related to the presence of bacterial toxins. Nucleic acids encoding a peptide of the invention can be used for the production of the peptides for diagnostic reagents, as vaccines and for therapies for pyrogenic exotoxin related diseases. Vectors expressing high levels of the peptides can be used in immunotherapy and immunoprophylaxis when expressed in humans. The antibodies are used for passive immunisation therapy to prevent or increase resistance to toxic shock syndrome or septic shock and to ameliorate the effects of conditions associated with the presence of staphylococcal or streptococcal pyrogenic toxins. The amino acid sequences of the peptides are sufficiently common that they can be used for eliciting antibodies which are cross-reactive with toxins derived from various bacteria. Sequences AA19783-197843 represent the synthetic peptides based on consensus consensus regions 1 and 2 of *Staphylococcus aureus* and Group A streptococcal pyrogenic toxins. These peptides can be administered to a mammal to raise serum antibodies for protection against or amelioration of toxic or septic shock.

Sequence 14 AA; SQ

Query Match	100.08;	Score 72;	DB 21;	Length 14;
Best Local Similarity	100.08;	Pred. No. 4.2e-06;		
Matches 12; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0

Qy	1	CMYGGVTEHEGN	12
Db	1	cmYgvtEhegn	12

Db 1 cm yg vtehegn 12

## RESULT 6

AAY72178  
ID AAY72178 standard; peptide; 14 AA.

AC AAY72178;

DT 24-APR-2001 (first entry)

Peptide #6344, derived from streptococcal and staphylococcal toxins.

KW Mononuclear cell; blastogenesis; inhibitor; HIV; replication; therapy;  
KW Tumor necrosis factor; human immunodeficiency virus; T cell;

streptococcal pyrogenic exotoxin; autoimmune disease; immunisation.

Streptococcus sp.

XX	W0300078790-A3
DN	

XX  
PD 28-DEC-2000

XX	16-TIN-2000: 2000WO-11516690
DE	

XX 18-JTN-1999. 99TTS-0336627  
PR

XX  
PA (LIVRO) INTY ROCKFEETLER

XX	visvanathan k	zabriskie ,TB
PI		

WPI: 2001-080820/09.

Providing protection

PT using peptides from homologous sequences of staphylococcal and immunodeficiency virus infections and associated deleterious effects,

XX  
F1 streptococcal

XX  
F3  
claim 3; Page 38; 10pp; English:

from the homologous sequences of staphylococcal enterotoxin and peptide #0344, a cross-linked polymer derived

CC The peptide, nucleic acid encoding the peptide and antibody (Ab) produced  
CC streptococcal pyrogenic exotoxin.

mononuclear cells

CC the effects of autoimmune diseases associated with the presence of HIV.  
CC The Ab is used for passively immunising a mammal against the deleterious  
CC effects of HIV.

Query Match	100.0%	Score 72	DB 22	Length 14
-------------	--------	----------	-------	-----------

Query Match

QY	1	CMYGVTEHEGN	12
Db	1	cmYgvtehegn	12

Db 1 cm ygvt ehegn 12

RESULT	7
AAW72426	
ID	AAW72426 standard; peptide; 36 AA

AAW72426;

DT 22-DEC-1998 (first entry)

Peptide #5 for reducing symptoms of toxic shock syndrome

KW Toxic shock syndrome; immunogenic response; bacterial infection;

staphylococcal enterotoxin; streptococcal pyrogenic toxin; antibody;

XX autoImmune disease.  
XX Synthetic.  
OS Staphylococcus sp.  
OS Streptococcus sp.  
XX MO9845325-A1.  
XX 15-OCT-1998.  
XX 01-APR-1998; 98WO-US06663.  
XX 07-APR-1997; 97US-0838413.  
XX (UVRQ ) UNIV ROCKEFELLER.  
XX Bannan JD, Zabriskie JB;  
XX MPI: 1998-56835/48.  
XX  
XX New peptides that generate antibodies against staphylococcal and  
PT streptococcal toxins - used to diagnose, treat or prevent toxic  
PT shock and autoImmune diseases  
XX  
XX Claim 4; Page 54; 69pp; English.  
XX  
XX The present invention describes peptides having consensus sequences #1  
CC or #2, optionally as part of a larger molecule of size at least 6-8 kD.  
CC Where consensus sequence #1 and #2 are: X25X26YGX17X23X4X5N #1,  
CC K6X78X9X10X11X12X13DX14X15X16RX17X18X27X19X20X21X22X23X24Y #2, where  
CC X1, X8, X13 and X24 = L, I or V; X3, X25 and X26 = any amino acid (aa)  
CC or are absent; X27 = L or Y; all other X may be any aa. The peptides  
CC can be used to generate serum antibodies (Ab) that bind at least one  
CC staphylococcal enterotoxin (SE) or streptococcal endotoxin (SE). Ab  
CC are used: (1) for diagnostic detection of SPEA or SEA, SEB and SED. In  
CC usual immunoassays; (11) to inhibit blastogenesis of human mononuclear  
CC cells in presence of these toxins (i.e. to protect against or alleviate  
CC toxic shock or autoImmune disease associated with bacterial infections);  
CC and (111) for passive immunisation against effects of the toxins. The  
CC peptides generate Ab that are cross-reactive with toxins from a variety  
CC of bacteria. The present sequence represents a specifically claimed  
CC example of a peptide of the present invention.  
XX  
XX Sequence 36 AA:  
SO

Query Match 100.0%; Score 72; DB 19; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1.2e-05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CMYGYTFHEGN 12  
Db 1 cmygytfehgn 12  
1 |||||||||

RESULT 8  
AA97842  
ID AA97842 standard; peptide: 36 AA.  
XX  
XX AA97842;  
XX  
XX 29-AUG-2000 (first entry)  
XX  
XX Staphylococcal/streptococcal pyrogenic toxin-derived peptide, 6347.  
XX  
XX Pyrogenic exotoxin; enterotoxin; streptococcal infection;  
XX staphylococcal infection; septic shock; toxic shock; vaccine;  
XX antibody.  
XX  
XX Synthetic.  
OS Staphylococcus aureus.  
OS Streptococcus sp. 'Group A'.  
XX

PN WO200020598-A1.  
XX  
XX 13-APR-2000.  
XX  
XX 24-SEP-1999; 99WO-US22180.  
XX  
XX 07-OCT-1998; 98US-0168303.  
XX 18-JUN-1999; 99US-0335581.  
XX  
XX (UVRQ ) UNIV ROCKEFELLER.  
XX  
XX Bannan JD, Viswanathan K, Zabriskie JB;  
XX MPI: 2000-303782/26.  
XX  
XX  
XX Peptides useful for preventing and reducing the symptoms of toxic shock  
PT syndrome and septic shock from staphylococcal and streptococcal  
PT infections -  
XX  
XX Claim 4; Page 86; 115pp; English.  
XX  
XX The invention relates to novel peptides (AA97838-97843) comprising a  
CC consensus amino acid sequence derived from two conserved regions  
CC (regions 1 and 2) of Staphylococcus aureus enterotoxins and  
CC streptococcal pyrogenic toxins. Consensus region 1a (a preferred  
CC consensus region 1) has the sequence X25-X26-Y-G-X1-T-X2-X3-X4-X5-N  
CC (AA97863) and consensus region 2a (a preferred consensus region 2) has  
CC the sequence K-X6-X7-X8  
CC X9-X10-X11-X12-X13-D-X14-X15-X16-R-X17-X18-X27-X19-X20-X21-X22-X23-X24-Y  
CC (AA97864), where: X1, X8, X13 and X24 are each independently selected  
CC from L, I and V; X2, X4, X5, X6, X7, X9, X10, X11, X12, X14, X15, X16,  
CC X17, X18, X19, X20, X21, X22 and X23 are each independently selected from  
CC the group consisting of any amino acid;  
CC X3, X5 and X26 are each independently selected from the group consisting  
CC of any amino acid and of no amino acid;  
CC X27 is either L or Y.  
CC The invention also relates to serum antibodies induced by the peptides  
CC which provide protection against, or reduce the severity of toxic shock  
CC and septic shock caused by the staphylococcal and streptococcal  
CC pyrogenic toxins. The pyrogenic exotoxins of Group A streptococci and  
CC the enterotoxins of Staphylococcus aureus (which are also pyrogenic  
CC exotoxins) constitute a family of structurally related toxins which  
CC share similar biological activities. They stimulate CD4+, CD8+ and  
CC gamma-delta+ T-cells by binding the beta-chain variable region (V-beta)  
CC elements on the lateral face of the T-cell receptor (TCR) while  
CC simultaneously binding the lateral face of the class II major  
CC histocompatibility complex (MHC) of antigen presenting cells. This causes  
CC aberrant proliferation of T-cells, which stimulates other components of  
CC the immune system, causing injury to the host. The peptides are used to  
CC prevent, treat or protect against toxic shock and septic shock resulting  
CC from bacterial infections in mammals, particularly humans. The peptides  
CC are used for inducing serum antibodies that bind at least one  
CC staphylococcal enterotoxin or streptococcal exotoxin and both the  
CC peptides and antibodies can be used in diagnostic assays to aid in the  
CC diagnosis of disease related to the presence of bacterial toxins. Nucleic  
CC acids encoding a peptide of the invention can be used for the production  
CC of the peptides for diagnostic reagents, as vaccines and for therapies  
CC for pyrogenic exotoxin related diseases. Vectors expressing high levels  
CC of the peptides can be used in immunotherapy and immunoprophylaxis when  
CC expressed in humans. The antibodies are used for passive immunisation  
CC therapy to prevent or increase resistance to toxic shock syndrome or  
CC septic shock and to ameliorate the effects of conditions associated with  
CC the presence of staphylococcal or streptococcal pyrogenic toxins. The  
CC amino acid sequences of the peptides are sufficiently common that they  
CC can be used for eliciting antibodies which are cross-reactive with toxins  
CC derived from various bacteria. Sequences AA97838-97843 represent the  
CC synthetic peptides based on consensus consensus regions 1 and 2 of  
CC Staphylococcus aureus and Group A streptococcal pyrogenic toxins.  
CC These peptides can be administered to a mammal to raise serum antibodies  
CC for protection against or amelioration of toxic or septic shock.  
XX  
XX Sequence 36 AA:  
SO

Query Match 100.0%; Score 72; DB 21; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CMYGVTEHEGN 12  
 |||||||||  
 Db 1 cmgyvtehegn 12

## RESULT 9

AAV72180  
 ID AAV72180 standard; peptide; 36 AA.

XX AC AAV72180;

DT 24-APR-2001 (first entry)

DE Peptide #6347, derived from streptococcal and staphylococcal toxins.

XX Mononuclear cell; blastogenesis; inhibitor: HIV; replication; therapy;

KM staphylococcal enterotoxin; human immunodeficiency virus; T cell;

XX streptococcal pyrogenic exotoxin; autoimmune disease; immunisation.

OS Streptococcus sp.

XX Staphylococcus sp.

PN WO200078790-A2.

PD 28-DEC-2000.

PF 16-JUN-2000; 2000WO-US16680.

PR 18-JUN-1999; 99US-0336627.

PA (UYRQ ) UNIV ROCKEFELLER.

PI Visvanathan K, Zabriskie JB;

DR WPI; 2001-080820/09.

XX Providing protection against, and reducing the severity of, human

PT immunodeficiency virus infections and associated deleterious effects,

XX using peptides from homologous sequences of staphylococcal and

PT streptococcal toxins

XX Claim 5; Page 38; 76pp; English.

XX The present sequence is peptide #6347, derived from the homologous

CC sequences of staphylococcal enterotoxin and streptococcal pyrogenic

CC exotoxin.

CC The peptide, nucleic acid encoding the peptide and antibody (Ab) produced

CC against the peptide are useful for inhibiting blastogenesis of

CC mononuclear cells (eg. T cells) in the presence of human immunodeficiency

CC virus (HIV), inhibiting HIV replication and protecting a mammal against

CC the deleterious effects of HIV. The peptide is also used to ameliorate

CC the effects of autoimmune diseases associated with the presence of HIV.

CC The Ab is used for passively immunising a mammal against the deleterious

CC effects of HIV.

XX Sequence 36 AA;

XX Query Match 100.0%; Score 72; DB 22; Length 36;

XX Best Local Similarity 100.0%; Pred. No. 1.2e-05;

XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CMYGVTEHEGN 12  
 |||||||||  
 Db 1 cmgyvtehegn 12

RESULT 10

AAW72427  
 ID AAW72427 standard; peptide; 38 AA.

XX AC AAW72427;

DT 22-DEC-1998 (first entry)

DE Peptide #6 for reducing symptoms of toxic shock syndrome.

XX Toxic shock syndrome; immunogenic response; bacterial infection;

KM staphylococcal enterotoxin; streptococcal pyrogenic toxin; antibody;

XX autoimmune disease.

XX Synthetic.

OS Staphylococcus sp.

XX Streptococcus sp.

PN WO9845325-A1.

PD 15-OCT-1998.

PF 01-APR-1998; 98WO-US06663.

PR 07-APR-1997; 97US-0838413.

PA (UYRQ ) UNIV ROCKEFELLER.

PI Bannan JD, Zabriskie JB;

DR WPI; 1998-568335/48.

XX New peptides that generate antibodies against staphylococcal and

PT streptococcal toxins - used to diagnose, treat or prevent toxic

PT shock and autoimmune diseases

XX Claim 4; Page 54; 69pp; English.

XX The present invention describes peptides having consensus sequences #1

CC or #2, optionally as part of a larger molecule of size at least 6-8 kD.

CC Where consensus sequence #1 and #2 are: X25X26YGX1X2X3X4X5N #1,

CC X6X7X8X9X10X11X12X13DX14X15X16RX17X18X27X19X20X21X22X23X24Y #2, where

CC X1, X8, X13 and X24 = L, I or V; X3, X25 and X26 = any amino acid (aa)

CC or are absent; X27 = L or Y; all other X may be any aa. The peptides

CC can be used to generate serum antibodies (Ab) that bind at least one

CC staphylococcal enterotoxin (SE) or streptococcal endotoxin (SPE). Ab

CC are used: (i) for diagnostic detection of SPEA or SPE, SEB and SED, in

CC usual immunoassays; (ii) to inhibit blastogenesis of human mononuclear

CC cells in presence of these toxins (i.e. to protect against or alleviate

CC toxic shock or autoimmune disease associated with bacterial infections);

CC and (iii) for passive immunisation against effects of the toxins. The

CC peptides generate Ab that are cross-reactive with toxins from a variety

CC of bacteria. The present sequence represents a specifically claimed

CC example of a peptide of the present invention.

XX Sequence 38 AA;

XX Query Match 100.0%; Score 72; DB 19; Length 38;

XX Best Local Similarity 100.0%; Pred. No. 1.2e-05;

XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CMYGVTEHEGN 12  
 |||||||||  
 Db 1 cmgyvtehegn 12

RESULT 11

AAV97843  
 ID AAV97843 standard; peptide; 38 AA.

XX AC AAV97843;

XX DT 29-AUG-2000 (first entry)

XX Staphylococcal/streptococcal pyrogenic toxin-derived peptide, 6348.  
DE  
XX  
KW Pyrogenic exotoxin; enterotoxin; streptococcal infection;  
KW staphylococcal infection; septic shock; toxic shock; vaccine;  
KW antibody.  
OS Synthetic.  
OS Staphylococcus aureus.  
OS Streptococcus sp. 'Group A'.  
PN MO200020598-X1.  
XX  
XX  
PD 13-APR-2000.  
XX  
PF 24-SEP-1999; 99WO-US22180.  
PR 07-OCT-1998; 98US-0168303.  
PR 18-JUN-1999; 99US-033581I.  
XX  
PA (UYRO ) UNIV ROCKEFELLER.  
PI Bannan JD, Visvanathan K, Zabriskie JB;  
XX WPI: 2000-303782/26.  
DR  
XX  
PT Peptides useful for preventing and reducing the symptoms of toxic shock  
PT syndrome and septic shock from staphylococcal and streptococcal  
PT infections -  
PS  
XX  
PS Claim 4; Page 88; 115pp; English.

The invention relates to novel peptides (AY97838-Y97843) comprising a consensus amino acid sequence derived from two conserved regions (regions 1 and 2) of Staphylococcus aureus enterotoxins and streptococcal pyrogenic toxins. Consensus region 1a (a preferred consensus region 1) has the sequence X25-X26-Y-G-G-X1-T-X2-X3-X4-X5-N (AY97863) and consensus region 2a (a preferred consensus region 2) has the sequence K-X6-X7-X8-X9-X10-X11-X12-X13-D-X14-X15-X16-R-X17-X18-X27-X19-X20-X21-X22-X23-X24-Y (AY97864), where: X1, X8, X13 and X24 are each independently selected from L, I and V; X2, X4, X5, X6, X7, X9, X10, X11, X12, X14, X15, X16, X17, X18, X19, X20, X21, X22 and X23 are each independently selected from the group consisting of any amino acid; X3, X5 and X26 are each independently selected from the group consisting of any amino acid and of no amino acid; X27 is either L or Y.

The invention also relates to serum antibodies induced by the peptides which provide protection against, or reduce the severity of toxic shock and septic shock caused by the staphylococcal and streptococcal pyrogenic toxins. The pyrogenic exotoxins of Group A streptococci and the enterotoxins of Staphylococcus aureus (which are also pyrogenic exotoxins) constitute a family of structurally related toxins which share similar biological activities. They stimulate CD4+, CD8+ and gamma-delta+ T-cells by binding the beta-chain variable region (V-beta) elements on the lateral face of the T-cell receptor (TCR) while simultaneously binding the lateral face of the class II major histocompatibility complex (MHC) of antigen presenting cells. This causes aberrant proliferation of T-cells, which stimulates other components of the immune system, causing injury to the host. The peptides are used to prevent, treat or protect against toxic shock and septic shock resulting from bacterial infections in mammals, particularly humans. The peptides are used for inducing serum antibodies that bind at least one staphylococcal enterotoxin or streptococcal exotoxin and both the peptides and antibodies can be used in diagnostic assays to aid in the diagnosis of disease related to the presence of bacterial toxins. Nucleic acids encoding a peptide of the invention can be used for the production of the peptides for diagnostic reagents, as vaccines and for therapies for pyrogenic exotoxin related diseases. Vectors expressing high levels of the peptides can be used in immunotherapy and immunoprophylaxis when expressed in humans. The antibodies are used for passive immunisation therapy to prevent or increase resistance to toxic shock syndrome or septic shock and to ameliorate the effects of conditions associated with

CC	the presence of staphylococcal or streptococcal pyrogenic toxins. The
CC	amino acid sequences of the peptides are sufficiently common that they
CC	can be used for eliciting antibodies which are cross-reactive with toxins
CC	derived from various bacteria. Sequences AAY97838-V978343 represent the
CC	synthetic peptides based on consensus consensus regions 1 and 2 of
CC	Staphylococcus aureus and Group A streptococcal pyrogenic toxins.
CC	These peptides can be administered to a mammal to raise serum antibodies
CC	for protection against or amelioration of toxic or septic shock.
XX	
SQ	Sequence    38 AA:
QY	Query Match                      100.0%; Score 72; DB 21; Length 38;
	Best Local Similarity         100.0%; Pred. No. 1.2e-05;
Matches	12; Conservative         0; Mismatches         0; Indels         0; Gaps         0;
	1 CMYGVTETHEGN 12
Dd	1 cmysgvtetehgn 12
RESULT	12
ID	AAY72181
AC	AAY72181 standard; peptide: 38 AA.
XX	
XX	AAY72181;
DT	
XX	24-APR-2001 (first entry)
DE	
XX	Peptide #6348, derived from streptococcal and staphylococcal toxins.
KM	Mononuclear cell; blastogenesis; inhibitor; HIV; replication; therapy;
KW	staphylococcal enterotoxin; human immunodeficiency virus; T cell;
XX	streptococcal pyrogenic exotoxin; autoimmune disease; immunisation.
OS	
OS	Streptococcus sp.
XX	Staphylococcus sp.
PM	
XX	WO200078790-A2.
PD	
XX	28-DEC-2000.
Pf	
XX	16-JUN-2000; 2000WO-US16680.
PR	
XX	18-JUN-1999; 99US-0336627.
PA	
XX	(UYRQ ) UNIV ROCKEFELLER.
PI	
XX	Visvanathan K, Zabrliske JB;
DR	
XX	WPI. 2001-080820/09.
PT	
XX	providing protection against, and reducing the severity of, human
PT	immunodeficiency virus infections and associated deleterious effects,
PT	using peptides from homologous sequences of staphylococcal and
PT	streptococcal toxins -
PS	
XX	Claim 5; Page 38; 76pp; English.
XX	
CC	The present sequence is peptide #6348, a cross-linked polymer derived
CC	from the homologous sequences of staphylococcal enterotoxin and
CC	streptococcal pyrogenic exotoxin.
CC	The peptide, nucleic acid encoding the peptide and antibody (Ab) produced
CC	against the peptide are useful for inhibiting blastogenests of
CC	mononuclear cells (eg. T cells) in the presence of human immunodeficiency
CC	virus (HIV), inhibiting HIV replication and protecting a mammal against
CC	the deleterious effects of HIV. The peptide is also used to ameliorate
CC	the effects of autoimmune diseases associated with the presence of HIV.
CC	The Ab is used for passively immunising a mammal against the deleterious
CC	effects of HIV.
XX	
XX	Sequence    38 AA:

Query Match 100.0%; Score 72; DB 22; Length 38;  
Best Local Similarity 100.0%; Pred. No. 1.2e-05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CMYGVTEHEGN 12  
Db 1 cmYgvttehgn 12  
|||||

RESULT 13  
AAV97845  
ID AAV97845 standard; peptide; 12 AA.  
AC AAV97845;  
XX 29-AUG-2000 (first entry)  
DT  
XX Staphylococcus aureus enterotoxin SEB, conserved region 1.  
DE  
XX Staphylococcal infection; enterotoxin; septic shock; toxic shock;  
KW vaccine; antibody.  
XX  
XX Staphylococcus aureus.  
OS  
XX WO200020598-A1.  
PN 13-APR-2000.  
PD  
XX 24-SEP-1999; 99WO-US22180.  
PZ  
XX 07-OCT-1998; 98US-0168303.  
PR 18-JUN-1999; 99US-0335581.  
XX  
XX (UTRQ ) UNIV ROCKEFELLER.  
PA  
XX Bannan JD, Visvanathan K, Zabriskie JB;  
PI  
XX WPI: 2000-303782/26.  
DR  
XX  
XX Peptides useful for preventing and reducing the symptoms of toxic shock  
PT syndrome and septic shock from staphylococcal and streptococcal  
PT infections -  
XX  
XX Example 1; Page 72; 115pp; English.  
PS  
XX The invention relates to novel peptides (AAV97838-Y97843) comprising a  
CC consensus amino acid sequence derived from two conserved regions  
CC (regions 1 and 2) of Staphylococcus aureus enterotoxins and  
CC streptococcal pyrogenic toxins. Consensus region 1a (a preferred  
CC consensus region 1) has the sequence X25-X26-Y-G-X1-T-X2-X3-X4-X5-N  
CC (AAV97863) and consensus region 2a (a preferred consensus region 2) has  
CC the sequence K-X6-X7-X8-  
CC X9-X10-X11-X12-X13-D-X14-X15-X16-R-X17-X18-X19-X20-X21-X22-X23-X24-Y  
CC (AAV97864), where: X1, X8, X13 and X24 are each independently selected  
CC from L, I and V; X2, X4, X5, X6, X7, X9, X10, X11, X12, X14, X15, X16,  
CC X17, X18, X19, X20, X21, X22 and X23 are each independently selected from  
CC the group consisting of any amino acid;  
CC X3, X5 and X26 are each independently selected from the group consisting  
CC of any amino acid and of no amino acid;  
CC X27 is either L or Y.  
CC The invention also relates to serum antibodies induced by the peptides  
CC which provide protection against, or reduce the severity of toxic shock  
CC and septic shock caused by the staphylococcal and streptococcal  
CC pyrogenic toxins. The pyrogenic exotoxins of Group A streptococci and  
CC the enterotoxins of Staphylococcus aureus (which are also pyrogenic  
CC exotoxins) constitute a family of structurally related toxins which  
CC share similar biological activities. They stimulate CD4+, CD8+ and  
CC gamma-delta+ T-cells by binding the beta-chain variable region (V-beta)  
CC elements on the lateral face of the T-cell receptor (TCR) while  
CC simultaneously binding the lateral face of the class II major  
CC histocompatibility complex (MHC) of antigen presenting cells. This causes  
CC aberrant proliferation of T-cells, which stimulates other components of

CC the immune system, causing injury to the host. The peptides are used to  
CC prevent, treat or protect against toxic shock and septic shock resulting  
CC from bacterial infections in mammals, particularly humans. The peptides  
CC are used for inducing serum antibodies that bind at least one  
CC staphylococcal enterotoxin or streptococcal exotoxin and both the  
CC peptides and antibodies can be used in diagnostic assays to aid in the  
CC diagnosis of disease related to the presence of bacterial toxins. Nucleic  
CC acids encoding a peptide of the invention can be used for the production  
CC of the peptides for diagnostic reagents, as vaccines and for therapies  
CC for pyrogenic exotoxin related diseases. Vectors expressing high levels  
CC of the peptides can be used in immunotherapy and immunoprophylaxis when  
CC expressed in humans. The antibodies are used for passive immunisation  
CC therapy to prevent or increase resistance to toxic shock syndrome or  
CC septic shock and to ameliorate the effects of conditions associated with  
CC the presence of staphylococcal or streptococcal pyrogenic toxins. The  
CC amino acid sequences of the peptides are sufficiently common that they  
CC can be used for eliciting antibodies which are cross-reactive with toxins  
CC derived from various bacteria. Sequences AAV97844-Y97852 represent  
CC conserved region 1 of various staphylococcus aureus enterotoxins and  
CC Group A streptococci pyrogenic exotoxins.  
XX  
XX Sequence 12 AA:  
SQ

Query Match 93.1%; Score 67; DB 21; Length 12;  
Best Local Similarity 91.7%; Pred. No. 2.6e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGVTEHEGN 12  
Db 1 cmYgvttehgn 12  
|||||

RESULT 14  
AAV97846  
ID AAV97846 standard; peptide; 12 AA.  
XX  
XX AAV97846;  
AC  
XX 29-AUG-2000 (first entry)  
DT  
XX Staphylococcus aureus enterotoxin SEC, conserved region 1.  
DE  
XX Staphylococcal infection; enterotoxin; septic shock; toxic shock;  
KW vaccine; antibody.  
XX  
XX Staphylococcus aureus.  
OS  
XX WO200020598-A1.  
PN 13-APR-2000.  
PD  
XX 24-SEP-1999; 99WO-US22180.  
PZ  
XX 07-OCT-1998; 98US-0168303.  
PR 18-JUN-1999; 99US-0335581.  
XX  
XX (UTRQ ) UNIV ROCKEFELLER.  
PA  
XX Bannan JD, Visvanathan K, Zabriskie JB;  
PI  
XX WPI: 2000-303782/26.  
DR  
XX  
XX Peptides useful for preventing and reducing the symptoms of toxic shock  
PT syndrome and septic shock from staphylococcal and streptococcal  
PT infections -  
XX  
XX Example 1; Page 72; 115pp; English.  
PS  
XX The invention relates to novel peptides (AAV97838-Y97843) comprising a  
CC consensus amino acid sequence derived from two conserved regions  
CC (regions 1 and 2) of Staphylococcus aureus enterotoxins and  
CC streptococcal pyrogenic toxins. Consensus region 1a (a preferred







GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 2, 2002, 17:35:14 ; Search time 40.75 Seconds  
(without alignments)  
6.627 Million cell updates/sec

Title: US-09-335-581A-3

Perfect score: 72

Sequence: 1 CMYGVTEHEGN 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/2/1aa/PCIOS.COMB.pep:\*  
6: /cgn2\_6/ptodata/2/1aa/Backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	72	100.0	12	3	US-08-838-413A-3
2	72	100.0	14	3	US-08-838-413A-5
3	72	100.0	36	3	US-08-838-413A-7
4	72	100.0	38	3	US-08-838-413A-8
5	67	93.1	12	3	US-08-838-413A-10
6	67	93.1	12	3	US-08-838-413A-11
7	67	93.1	13	4	US-08-896-933-3
8	67	93.1	14	4	US-08-896-933-5
9	67	93.1	238	4	US-08-896-933-28
10	67	93.1	239	4	US-08-896-933-26
11	67	93.1	239	4	US-08-896-933-27
12	67	93.1	255	1	US-08-446-918A-2
13	67	93.1	255	1	US-08-580-806-2
14	64	88.9	14	4	US-08-896-933-13
15	64	88.9	220	4	US-08-896-933-20
16	63	87.5	12	3	US-08-838-413A-15
17	63	87.5	14	4	US-08-896-933-11
18	63	87.5	221	4	US-08-896-933-29
19	60	83.3	12	3	US-08-838-413A-12
20	60	83.3	14	4	US-08-896-933-7
21	60	83.3	228	4	US-08-896-933-25
22	59	81.9	12	3	US-08-838-413A-17
23	59	81.9	239	4	US-08-896-933-21
24	55	76.4	12	3	US-08-838-413A-9
25	55	76.4	12	3	US-08-838-413A-13
26	55	76.4	12	3	US-08-838-413A-30
27	55	76.4	14	4	US-08-896-933-1

28	55	76.4	14	4	US-08-896-933-9	Sequence 9, Appl1
29	55	76.4	23	1	US-08-220-378-5	Sequence 5, Appl1
30	55	76.4	23	2	US-08-696-012-5	Sequence 5, Appl1
31	55	76.4	226	4	US-08-896-933-24	Sequence 24, Appl1
32	55	76.4	232	4	US-08-896-933-23	Sequence 23, Appl1
33	55	76.4	233	4	US-08-446-918A-4	Sequence 4, Appl1
34	55	76.4	233	2	US-08-580-806-4	Sequence 4, Appl1
35	55	76.4	257	3	US-08-486-099-112	Sequence 112, App
36	55	76.4	257	3	US-08-486-099-113	Sequence 113, App
37	55	76.4	257	3	US-08-360-107A-122	Sequence 122, App
38	55	76.4	257	3	US-08-360-107A-123	Sequence 123, App
39	55	76.4	257	3	US-08-484-223B-112	Sequence 112, App
40	55	76.4	257	3	US-08-484-223B-113	Sequence 113, App
41	55	76.4	257	3	US-08-919-597-112	Sequence 112, App
42	55	76.4	257	3	US-08-919-597-113	Sequence 113, App
43	55	76.4	257	3	US-08-475-668A-112	Sequence 112, App
44	55	76.4	257	3	US-08-475-668A-113	Sequence 113, App
45	55	76.4	257	3	US-08-485-551A-112	Sequence 112, App

#### ALIGNMENTS

RESULT 1  
US-08-838-413A-3  
; Sequence 3, Application US/08838413A  
; Patent No. 6075119  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: PEPTIDES USEFUL FOR  
; TITLE OR INVENTION: REDUCING SYMPTOMS OF TOXIC SHOCK SYNDROME  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: MORGAN & FINNEGAN  
; STREET: 345 PARK AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10154  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: FLOPPY DISK  
; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WORDPERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/838,413A  
; FILING DATE: 07-APR-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MORRY, MARY J.  
; REGISTRATION NUMBER: 34,398  
; REFERENCE/DOCKET NUMBER: 2016-4010  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)758-4800  
; TELEFAX: (212)751-6849  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12  
; TYPE: AMINO ACID  
; STRANDEDNESS: UNKNOWN  
; TOPOLOGY: UNKNOWN  
; MOLECULE TYPE: PEPTIDE  
; US-08-838-413A-3  
Query Match 100.0%; Score 72; DB 3; Length 12;  
Best local Similarity 100.0%; Pred. No. 4.1e-06;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CMYGVTEHEGN 12  
|||||  
Db 1 CMYGVTEHEGN 12

## RESULT 2

US-08-838-413A-5  
; Sequence 5, Application us/08838413A  
; Patent No. 6075119  
; GENERAL INFORMATION:

APPLICANT:

APPLICANT:

TITLE OF INVENTION: PEPTIDES USEFUL FOR

TITLE OF INVENTION: REDUCING SYMPTOMS OF TOXIC SHOCK SYNDROME

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN

STREET: 345 PARK AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/838,413A

FILING DATE: 07-APR-1997

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: MORRY, MARY J.

REGISTRATION NUMBER: 34,398

REFERENCE/DOCKET NUMBER: 2016-4010

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)751-6849

TELEFAX: (212)751-6849

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 14

TYPE: AMINO ACID

STRANDEDNESS: UNKNOWN

TOPOLOGY: UNKNOWN

MOLECULE TYPE: PEPTIDE

US-08-838-413A-5

Query Match

Best Local Similarity 100.0%; Score 72; DB 3; Length 14;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CMYGVTEHEGN 12

Db 1 CMYGVTEHEGN 12

## RESULT 3

US-08-838-413A-7

; Sequence 7, Application us/08838413A

; Patent No. 6075119

; GENERAL INFORMATION:

APPLICANT:

APPLICANT:

TITLE OF INVENTION: PEPTIDES USEFUL FOR

TITLE OF INVENTION: REDUCING SYMPTOMS OF TOXIC SHOCK SYNDROME

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN

STREET: 345 PARK AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/838,413A

FILING DATE: 07-APR-1997

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: MORRY, MARY J.

REGISTRATION NUMBER: 34,398

REFERENCE/DOCKET NUMBER: 2016-4010

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)751-6849

TELEFAX: (212)751-6849

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 36

TYPE: AMINO ACID

STRANDEDNESS: UNKNOWN

TOPOLOGY: UNKNOWN

MOLECULE TYPE: PEPTIDE

US-08-838-413A-7

Query Match

Best Local Similarity 100.0%; Score 72; DB 3; Length 36;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CMYGVTEHEGN 12

Db 1 CMYGVTEHEGN 12

## RESULT 4

US-08-838-413A-8

; Sequence 8, Application us/08838413A

; Patent No. 6075119

; GENERAL INFORMATION:

APPLICANT:

APPLICANT:

TITLE OF INVENTION: PEPTIDES USEFUL FOR

TITLE OF INVENTION: REDUCING SYMPTOMS OF TOXIC SHOCK SYNDROME

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN

STREET: 345 PARK AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/838,413A

FILING DATE: 07-APR-1997

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: MORRY, MARY J.

REGISTRATION NUMBER: 34,398

REFERENCE/DOCKET NUMBER: 2016-4010

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)751-6849

TELEFAX: (212)751-6849

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 36

TYPE: AMINO ACID

STRANDEDNESS: UNKNOWN

TOPOLOGY: UNKNOWN

MOLECULE TYPE: PEPTIDE

US-08-838-413A-8

Query Match

Best Local Similarity 100.0%; Score 72; DB 3; Length 36;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CMYGVTEHEGN 12

Db 1 CMYGVTEHEGN 12

;; FILING DATE:  
;; CLASSIFICATION: 536  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: MORRY, MARY J.  
;; REGISTRATION NUMBER: 34,398  
;; REFERENCE/DOCKET NUMBER: 2016-4010  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (212)751-6849  
;; TELEFAX: (212)751-6849  
;; INFORMATION FOR SEQ ID NO: 8:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 38  
;; TYPE: AMINO ACID  
;; STRANDEDNESS: UNKNOWN  
;; TOPOLOGY: UNKNOWN  
;; MOLECULE TYPE: PEPTIDE  
;; US-08-838-413A-8

Query Match 100.0%; Score 72; DB 3; Length 38;  
Best Local Similarity 100.0%; Pred. No. 1,4e-05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CMYGGVTEHGN 12  
Db 1 CMYGGVTEHGN 12

RESULT 5  
US-08-838-413A-10  
; Sequence 10, Application US/08838413A  
; Patent No. 6075119  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: PEPTIDES USEFUL FOR  
; TITLE OF INVENTION: REDUCING SYMPTOMS OF TOXIC SHOCK SYNDROME  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORGAN & FINNEGAN  
; STREET: 345 PARK AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10154  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: FLOPPY DISK  
; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WORDPERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/838,413A  
; FILING DATE: 07-APR-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MORRY, MARY J.  
; REGISTRATION NUMBER: 34,398  
; REFERENCE/DOCKET NUMBER: 2016-4010  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)751-6849  
; TELEFAX: (212)751-6849  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12  
; TYPE: AMINO ACID  
; STRANDEDNESS: UNKNOWN  
; TOPOLOGY: UNKNOWN  
; MOLECULE TYPE: PEPTIDE  
; US-08-838-413A-10

Query Match 93.1%; Score 67; DB 3; Length 12;  
Best Local Similarity 91.7%; Pred. No. 2.8e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 CMYGGVTEHGN 12  
Db 1 CMYGGVTEHGN 12

RESULT 6  
US-08-838-413A-11  
; Sequence 11, Application US/08838413A  
; Patent No. 6075119  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: PEPTIDES USEFUL FOR  
; TITLE OF INVENTION: REDUCING SYMPTOMS OF TOXIC SHOCK SYNDROME  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORGAN & FINNEGAN  
; STREET: 345 PARK AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10154  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: FLOPPY DISK  
; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WORDPERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/838,413A  
; FILING DATE: 07-APR-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MORRY, MARY J.  
; REGISTRATION NUMBER: 34,398  
; REFERENCE/DOCKET NUMBER: 2016-4010  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)751-6849  
; TELEFAX: (212)751-6849  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12  
; TYPE: AMINO ACID  
; STRANDEDNESS: UNKNOWN  
; TOPOLOGY: UNKNOWN  
; MOLECULE TYPE: PEPTIDE  
; US-08-838-413A-11

Query Match 93.1%; Score 67; DB 3; Length 12;  
Best Local Similarity 83.3%; Pred. No. 2.8e-05;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CMYGGVTEHGN 12  
Db 1 CMYGGVTEHGN 12

RESULT 7  
US-08-896-933-3  
; Sequence 3, Application US/08896933  
; Patent No. 6221351  
; GENERAL INFORMATION:  
; APPLICANT: Terman, David S.

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; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,  
; FILE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS  
; FILE REFERENCE: 09629/005002  
; CURRENT APPLICATION NUMBER: US/08/896,933  
; CURRENT FILING DATE: 1997-07-18  
; EARLIER FILING DATE: 1994-06-02  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 3  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Staphylococcus aureas  
US-08-896-933-3
```

```
Query Match          93.1%; Score 67; DB 4; Length 13;  
Best Local Similarity 91.7%; Pred. No. 3e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      1 CMYGGVTEHGN 12  
        |||||:|||||  
Db      1 CMYGGVTEHGN 12
```

```
RESULT      8  
US-08-896-933-5  
; Sequence 5, Application US/08896933  
; Patent No. 6221351  
; GENERAL INFORMATION:  
; APPLICANT: Terman, David S.  
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,  
; FILE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS  
; FILE REFERENCE: 09629/005002  
; CURRENT APPLICATION NUMBER: US/08/896,933  
; CURRENT FILING DATE: 1997-07-18  
; EARLIER FILING DATE: 1994-06-02  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 5  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Staphylococcus aureas  
US-08-896-933-5
```

```
Query Match          93.1%; Score 67; DB 4; Length 14;  
Best Local Similarity 83.3%; Pred. No. 3.2e-05;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 CMYGGVTEHGN 12  
        |||||:|||||  
Db      1 CMYGGITKHEGN 12
```

```
RESULT      9  
US-08-896-933-28  
; Sequence 28, Application US/08896933  
; Patent No. 6221351  
; GENERAL INFORMATION:  
; APPLICANT: Terman, David S.  
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,  
; FILE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS  
; FILE REFERENCE: 09629/005002  
; CURRENT APPLICATION NUMBER: US/08/896,933  
; CURRENT FILING DATE: 1997-07-18  
; EARLIER FILING DATE: 1994-06-02  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 28  
; LENGTH: 238
```

```
; TYPE: PRT  
; ORGANISM: Staphylococcus aureas  
US-08-896-933-28
```

```
Query Match          93.1%; Score 67; DB 4; Length 238;  
Best Local Similarity 83.3%; Pred. No. 0.00061;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 CMYGGVTEHGN 12  
        |||||:|||||  
Db      109 CMYGGITKHEGN 120
```

```
RESULT      10  
US-08-896-933-26  
; Sequence 26, Application US/08896933  
; Patent No. 6221351  
; GENERAL INFORMATION:  
; APPLICANT: Terman, David S.  
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,  
; FILE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS  
; FILE REFERENCE: 09629/005002  
; CURRENT APPLICATION NUMBER: US/08/896,933  
; CURRENT FILING DATE: 1997-07-18  
; EARLIER FILING DATE: 1994-06-02  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 26  
; LENGTH: 239  
; TYPE: PRT  
; ORGANISM: Staphylococcus aureas  
US-08-896-933-26
```

```
Query Match          93.1%; Score 67; DB 4; Length 239;  
Best Local Similarity 91.7%; Pred. No. 0.00061;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      1 CMYGGVTEHGN 12  
        |||||:|||||  
Db      113 CMYGGVTEHGN 124
```

```
RESULT      11  
US-08-896-933-27  
; Sequence 27, Application US/08896933  
; Patent No. 6221351  
; GENERAL INFORMATION:  
; APPLICANT: Terman, David S.  
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,  
; FILE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS  
; FILE REFERENCE: 09629/005002  
; CURRENT APPLICATION NUMBER: US/08/896,933  
; CURRENT FILING DATE: 1997-07-18  
; EARLIER FILING DATE: 1994-06-02  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 27  
; LENGTH: 239  
; TYPE: PRT  
; ORGANISM: Staphylococcus aureas  
US-08-896-933-27
```

```
Query Match          93.1%; Score 67; DB 4; Length 239;  
Best Local Similarity 83.3%; Pred. No. 0.00061;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 CMYGGVTEHGN 12  
        |||||:|||||
```

DB 110 CMYGVTEHGN 121

RESULT 12

US-08-446-918A-2  
; Sequence 2, Application US/08446918A  
; Patent No. 5705151

GENERAL INFORMATION:

APPLICANT: Dow, Steve W.

APPLICANT: Elmslie, Robyn E.

TITLE OF INVENTION: GENE THERAPY FOR T CELL REGULATION

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sheridan Ross & McIntosh

STREET: 1700 Lincoln Street, Suite 3500

CITY: Denver

STATE: Colorado

COUNTRY: U.S.A.

ZIP: 80203

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/446,918A

FILING DATE: 18-MAY-1995

CLASSIFICATION: 552

ATTORNEY/AGENT INFORMATION:

NAME: Kovarik, Joseph E.

REGISTRATION NUMBER: 33,005

REFERENCE/DOCKET NUMBER: 2879-29

TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 863-9700

TELEFAX: (303) 863-0223

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 255 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-446-918A-2

Query Match 93.1%; Score 67; DB 1; Length 255;

Best Local Similarity 91.7%; Pred. No. 0.00065;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGVTEHGN 12

DB 129 CMYGVTEHGN 140

RESULT 13

US-08-580-806-2

Sequence 2, Application US/08580806

Patent No. 5935568

GENERAL INFORMATION:

APPLICANT: Dow, Steve W.

APPLICANT: Elmslie, Robyn E.

APPLICANT: Potter, Terence A.

TITLE OF INVENTION: GENE THERAPY FOR EFFECTOR CELL REGULATION

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sheridan Ross & McIntosh

STREET: 1700 Lincoln Street, Suite 3500

CITY: Denver

STATE: Colorado

COUNTRY: U.S.A.

ZIP: 80203

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/580,806  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Connell, Gary J.  
REGISTRATION NUMBER: 32,020  
REFERENCE/DOCKET NUMBER: 2879-29-C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 863-9700  
TELEFAX: (303) 863-0223  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 255 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-580-806-2

Query Match 93.1%; Score 67; DB 2; Length 255;

Best Local Similarity 91.7%; Pred. No. 0.00065;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGVTEHGN 12

DB 129 CMYGVTEHGN 140

RESULT 14

US-08-896-933-13

Sequence 13, Application US/08896933

Patent No. 6221351

GENERAL INFORMATION:

APPLICANT: Terman, David S.

TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,

FILE REFERENCE: 09629/005002

CURRENT APPLICATION NUMBER: US/08/896,933

CURRENT FILING DATE: 1997-07-18

EARLIER FILING DATE: 1994-06-02

NUMBER OF SEQ ID NOS: 34

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 13

LENGTH: 14

TYPE: PRT

ORGANISM: Other

FEATURE:

OTHER INFORMATION: Consensus sequences derived from staphylococcus

US-08-896-933-13

Query Match 88.9%; Score 64; DB 4; Length 14;

Best Local Similarity 91.7%; Pred. No. 0.0001;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGVTEHGN 12

DB 1 CMYGVTEHGN 12

RESULT 15

US-08-896-933-20

Sequence 20, Application US/08896933

Patent No. 6221351

GENERAL INFORMATION:

APPLICANT: Terman, David S.

TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,

US-08-896-933-20

Query Match 88.9%; Score 64; DB 4; Length 14;

Best Local Similarity 91.7%; Pred. No. 0.0001;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGVTEHGN 12

DB 1 CMYGVTEHGN 12

RESULT 15

US-08-896-933-20

Sequence 20, Application US/08896933

Patent No. 6221351

GENERAL INFORMATION:

APPLICANT: Terman, David S.

TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,

US-08-896-933-20

Query Match 88.9%; Score 64; DB 4; Length 14;

Best Local Similarity 91.7%; Pred. No. 0.0001;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGVTEHGN 12

DB 1 CMYGVTEHGN 12

```

; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; CURRENT FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 20
; LENGTH: 220
; TYPE: PR1
; ORGANISM: Streptococcus pyogenes
US-08-896-933-20
    
```

```

Query Match      88.9%; Score 64; DB 4; Length 220;
Best Local Similarity 83.3%; Pred. No. 0.0018;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 CMYGYTEHEGN 12
        1:||||| |||
Db      98 CLYGYTNEHGN 109
    
```

Search completed: January 2, 2002, 20:46:42  
 Job time: 11488 sec



GenCore version 4.5  
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## OM protein - protein search, using sw model

Run on: January 2, 2002, 20:36:20 ; Search time 56.72 Seconds

(without alignments)  
16.116 Million cell updates/sec

Title: US-09-335-581A-3

Perfect score: 72

Sequence: 1 CMGCGVTEHNGN 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR.68:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	67	93.1	266	1 ENSAB6	enterotoxin B prec
2	67	93.1	266	1 ENSAC1	enterotoxin C-1 pr
3	67	93.1	266	2 A60114	enterotoxin C-2 pr
4	67	93.1	266	2 S11885	enterotoxin C3 - S
5	64	88.9	250	1 A26152	streptococcal pyro
6	63	87.5	236	2 S18789	exotoxin A precus
7	63	87.5	236	2 S18786	exotoxin type A pr
8	63	87.5	236	2 S18783	exotoxin type A pr
9	63	87.5	251	1 S29659	exotoxin type A pr
10	60	83.3	258	2 A33953	enterotoxin D prec
11	55	76.4	257	2 A28664	enterotoxin A prec
12	55	76.4	257	2 A28179	enterotoxin E prec
13	46	63.9	270	2 B48826	high chorioleptic h
14	46	63.9	279	2 C48826	high chorioleptic h
15	45	62.5	366	2 T25259	hypothetical prote
16	45	62.5	375	2 T27314	hypothetical prote
17	42	58.3	203	2 T06277	MADS box protein A
18	41	56.9	151	2 S43727	hypothetical prote
19	41	56.9	644	2 D71427	receptor-like prot
20	41	56.9	664	2 T51247	ARR2 protein [limp
21	41	56.9	669	2 T51246	ARR1 protein [limp
22	40	55.6	185	2 S04792	mobilization prote
23	40	55.6	303	2 C34504	heterogeneous ribo
24	40	55.6	347	2 T35013	probable membrane
25	40	55.6	380	2 G01639	transmembrane prot
26	40	55.6	388	2 T09885	hypothetical prote
27	40	55.6	413	2 E65088	hypothetical prote
28	40	55.6	455	2 T15581	hypothetical prote
29	40	55.6	747	2 B83029	conserved hypotet

30	40	55.6	789	2 A82166	conserved hypotet
31	40	55.6	813	2 T40622	translation elonga
32	40	55.6	877	2 S65057	alpha-glucosidase
33	39	54.2	324	2 T26790	hypothetical prote
34	39	54.2	384	2 T19427	hypothetical prote
35	39	54.2	384	2 T19423	hypothetical prote
36	39	54.2	422	2 F75151	hypothetical prote
37	39	54.2	424	2 D71192	hypothetical prote
38	39	54.2	1827	2 T34288	hypothetical prote
39	38	52.8	198	2 S54733	ribosomal protein
40	38	52.8	242	2 S30238	finger protein ZNF
41	38	52.8	437	2 S69881	phosphopyruvate hy
42	38	52.8	437	2 S67305	phosphopyruvate hy
43	38	52.8	444	2 T15310	hypothetical prote
44	38	52.8	472	2 T45219	hypothetical prote
45	38	52.8	628	2 T09458	numb-binding prote

## ALIGNMENTS

```
RESULT 1
ENSAB6
enterotoxin B precursor - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 24-Apr-1984 #sequence_revision 15-Oct-1996 #text_change 18-Jun-1999
C:Accession: S27360; A92065; S27240; A01815
R:Jones, C.L.; Khan, S.A.
J. Bacteriol. 166, 29-33, 1986
A:Title: Nucleotide sequence of the enterotoxin B gene from Staphylococcus aureus.
A:Reference number: S27360; MUID:86168029
A:Accession: S27360
A:Molecule type: DNA
A:Residues: 1-266 <JON>
A:Cross-References: EMBL:M1118; NID:g152939; PIDN:AA88550.1; PID:g153000
R:Experimental source: strain S6
J. Huang, I.Y.; Bergdoll, M.S.
J. Biol. Chem. 245, 3518-3525, 1970
A:Title: The primary structure of staphylococcal enterotoxin B. III. The cyanogen bro
A:Reference number: A92065; MUID:71007902
A:Accession: A92065
A:Molecule type: Protein
A:Residues: 28-55, 'ND', 59-68, 'NE', 71, 'FDLIVL', 78-117, 119-127, 'N', 129, 'D', 131-132, 'EN
R:Experimental source: strain S-6
J. Huang, I.Y.; Bergdoll, M.S.
J. Biol. Chem. 245, 3511-3517, 1970
A:Title: The primary structure of staphylococcal enterotoxin B. II. Isolation, compos
A:Reference number: A92064; MUID:71007901
A:Contents: annotation: chymotryptic peptides
J. Huang, I.Y.; Bergdoll, M.S.
J. Biol. Chem. 245, 3493-3510, 1970
A:Title: The primary structure of staphylococcal enterotoxin B. I. Isolation, composi
A:Reference number: A92063; MUID:71007900
A:Contents: annotation: tryptic peptides
R:Schantz, E.J.; Roessler, W.G.; Wegman, J.; Spero, L.; Dunnery, D.A.; Bergdoll, M.S.
Biochemistry 4, 1011-1016, 1965
A:Title: Purification of staphylococcal enterotoxin B.
A:Reference number: A90548; MUID:66035792
A:Contents: annotation: Biological source of protein
R:Alakhov, V.Y.; Klinsky, E.Y.; Kolosov, M.I.; Maurer-Fogy, I.; Moskaleva, E.Y.; Sves
Eur. J. Biochem. 209, 823-828, 1992
A:Title: Identification of functionally active fragments of staphylococcal enterotoxi
A:Reference number: S27240; MUID:93049338
A:Accession: S27240
A:Molecule type: Protein
A:Residues: 28-42, 128-148 <ALA>
C:Superfamily: enterotoxin B
C:Keywords: enterotoxin; extracellular protein; toxin
F:1-27/Domain: signal sequence #status predicted <Sig>
F:28-266/Product: enterotoxin B #status experimental <Mat>
F:120-140/Disulfide bonds: #status experimental
```

Query Match 93.1%; Score 67; DB 1; Length 266;  
Best Local Similarity 91.7%; Pred. No. 0.00017;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGVTEHNGN 12  
DB 140 CMYGVTEHNGN 151

## RESULT 2

ENSAC1

enterotoxin C-1 precursor - Staphylococcus aureus

C:Species: Staphylococcus aureus

C:Date: 15-Nov-1984 #sequence\_revision 05-Jan-1996 #text\_change 18-Jun-1999

C:Accession: S06356; A01816

R:Bohach, G.A.; Schlievert, P.M.

Mol. Gen. Genet. 209, 15-20, 1987

A:Title: Nucleotide sequence of the staphylococcal enterotoxin C1 gene and relatedness

A:Reference number: S06356; MUID:88038352

A:Accession: S06356

A:Molecule type: DNA

A:Residues: 1-266 &lt;BOH&gt;

A:Cross-references: EMBL:X05815; NID:g46566; PIDN:CAA29260.1; PID:g46567

R:Schmidt, J.J.; Spero, L.

J. Biol. Chem. 258, 6300-6306, 1983

A:Title: The complete amino acid sequence of Staphylococcal enterotoxin C-1.

A:Reference number: A01816; MUID:83213327

A:Accession: A01816

A:Molecule type: protein

A:Residues: 28-75, 'IL', '78-176, 'N', '178-266 &lt;SCH&gt;

C:Genetics: A:gene: entC1

C:Superfamily: enterotoxin B

C:Keywords: enterotoxin

F:1-27/Domain: signal sequence #status predicted &lt;SIG&gt;

F:28-266/Product: enterotoxin C-1 #status experimental &lt;MAT&gt;

F:120-137/Disulfide bonds: #status experimental

Query Match 93.1%; Score 67; DB 1; Length 266;  
Best Local Similarity 83.3%; Pred. No. 0.00017;

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 CMYGVTEHNGN 12  
DB 137 CMYGVTEHNGN 148

## RESULT 3

enterotoxin C-2 precursor - Staphylococcus aureus

N:Alternate names: enterotoxin C-3 precursor

C:Species: Staphylococcus aureus

C:Date: 10-Nov-1992 #sequence\_revision 10-Nov-1992 #text\_change 16-Jul-1999

C:Accession: A60114; B60114; A13866

R:Bohach, G.A.; Schlievert, P.M.

Infect. Immun. 57, 2249-2252, 1989

A:Title: Conservation of the biologically active portions of staphylococcal enterotoxins

A:Reference number: A60114; MUID:89277549

A:Accession: A60114

A:Molecule type: DNA

A:Residues: 1-266 &lt;BOH&gt;

A:Accession: B60114

A:Molecule type: protein

A:Residues: 28-66 &lt;BOH2&gt;

R:Couch, J.L.; Betley, M.J.

J. Bacteriol. 171, 4507-4510, 1989

A:Title: Nucleotide sequence of the type C-3 staphylococcal enterotoxin gene suggests th

A:Reference number: A13866; MUID:89327174

A:Accession: A13866

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-266 <COH>  
A:Cross-references: GB:M28364; NID:g153003; PIDN:AAA26624.1; PID:g153004  
C:Genetics: A:gene: entC2  
C:Superfamily: enterotoxin B  
F:1-27/Domain: signal sequence #status predicted <SIG>  
F:28-266/Product: enterotoxin C-2 #status predicted <MAT>

Query Match 93.1%; Score 67; DB 2; Length 266;  
Best Local Similarity 83.3%; Pred. No. 0.00017;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 CMYGVTEHNGN 12  
DB 137 CMYGVTEHNGN 148

## RESULT 4

enterotoxin C3 - Staphylococcus aureus

C:Species: Staphylococcus aureus

C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 16-Jul-1999

C:Accession: S11885

R:Howde, C.J.; Hackett, S.P.; Bohach, G.A.

Mol. Gen. Genet. 220, 329-333, 1990

A:Title: Nucleotide sequence of the staphylococcal enterotoxin C3 gene: sequence comp

A:Reference number: S11885; MUID:90220508

A:Accession: S11885

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-266 &lt;HOV&gt;

A:Cross-references: GB:X51661; NID:g46570; PIDN:CAA35972.1; PID:g46571

C:Superfamily: enterotoxin B

Query Match 93.1%; Score 67; DB 2; Length 266;  
Best Local Similarity 83.3%; Pred. No. 0.00017;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 CMYGVTEHNGN 12  
DB 137 CMYGVTEHNGN 148

## RESULT 5

A26152

streptococcal pyrogenic exotoxin type A precursor - Streptococcus sp.

N:Alternate names: scarlet fever toxin; SPE type A (spear)

C:Species: Streptococcus sp.

C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999

C:Accession: A26152

R:Johnson, L.P.; L'Italien, J.J.; Schlievert, P.M.

Mol. Gen. Genet. 203, 354-356, 1986

A:Title: Streptococcal pyrogenic exotoxin type A (scarlet fever toxin) is related to

A:Reference number: A26152; MUID:86284313

A:Accession: A26152

A:Molecule type: DNA

A:Residues: 1-250 &lt;JOH&gt;

C:Superfamily: enterotoxin B

C:Keywords: exotoxin

Query Match 88.9%; Score 64; DB 1; Length 250;  
Best Local Similarity 83.3%; Pred. No. 0.00054;  
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGVTEHNGN 12  
DB 128 CLYGVTEHNGN 139

## RESULT 6

S18789  
A:Experimental source: strain MGAS262 isolate California  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991  
A:Accession: S18789  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Accession: S18789  
A:Molecule type: DNA  
A:Residues: 1-236 <NEU>  
A:Cross-references: EMBL:X61573; NID:q47303; PIDN:CAA43771.1; PID:q47304  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991  
C:Genetics:  
A:Gene: speA  
C:Superfamily: enterotoxin B  
C:Keywords: exotoxin  
F:1-22/Domain: signal sequence (fragment) #status predicted <SIG>  
F:23-236/Product: exotoxin A (fragment) #status predicted <MAT>  
  
Query Match 87.5%; Score 63; DB 2; Length 236;  
Best Local Similarity 83.3%; Pred. No. 0.00078;  
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
Oy 1 CMYGVTEHEGN 12  
1:||||| ||||  
Db 120 CTVGVTHNEGN 131  
  
RESULT 7  
S18786  
exotoxin type A precursor (allele 2) - Streptococcus pyogenes phage (strain MGAS250 isol  
N:Alternate names: scarlet fever toxin  
C:Species: Streptococcus pyogenes phage  
A:Variety: strain MGAS250 isolate California; strain MGAS251 isolate California; strain  
Isolate United Kingdom; strain MGAS496 isolate Germany  
C:Date: 29-Jan-1993 #sequence\_revision 29-Jan-1993 #text\_change 16-Jul-1999  
R:Accession: S18786; S18787; S18788; S18790; S18792; S18795; S18799  
R:Nelson, K.; Schlievert, P.M.; Seldner, R.K.; Musser, J.M.  
J. Exp. Med. 174, 1271-1274, 1991  
A:Title: Characterization and clonal distribution of four alleles of the speA gene encod  
A:Reference number: S18782; MUID:92044323  
A:Accession: S18786  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-236 <NEU>  
A:Cross-references: EMBL:X61561; NID:q47297; PIDN:CAA43759.1; PID:q47298  
A:Experimental source: strain MGAS250 isolate California unassigned phage  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991  
A:Accession: S18787  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-236 <NEU>  
A:Cross-references: EMBL:X61562; NID:q47299; PIDN:CAA43760.1; PID:q47300  
A:Experimental source: strain MGAS251 isolate California unassigned phage  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991  
A:Accession: S18788  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-236 <NEU>  
A:Cross-references: EMBL:X61563; NID:q47301; PIDN:CAA43761.1; PID:q47302  
A:Experimental source: strain MGAS256 isolate California unassigned phage  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991  
A:Accession: S18790  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-236 <NEU>  
A:Cross-references: EMBL:X61564; NID:q47305; PIDN:CAA43762.1; PID:q47306

A:Experimental source: strain MGAS285 isolate Colorado unassigned phage  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199  
A:Accession: S18792  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-236 <NEU>  
A:Cross-references: EMBL:X61565; NID:q47311; PIDN:CAA43763.1; PID:q47312  
A:Experimental source: strain MGAS480 isolate Yugoslavia unassigned phage  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199  
A:Accession: S18795  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-236 <NEU>  
A:Cross-references: EMBL:X61566; NID:q47317; PIDN:CAA43764.1; PID:q47318  
A:Experimental source: strain MGAS492 isolate United Kingdom unassigned phage  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199  
A:Accession: S18799  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-236 <NEU>  
A:Cross-references: EMBL:X61567; NID:q47325; PIDN:CAA43765.1; PID:q47326  
A:Experimental source: strain MGAS496 isolate Germany unassigned phage  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199  
C:Genetics:  
A:Gene: speA2  
C:Superfamily: enterotoxin B  
C:Keywords: exotoxin  
F:1-22/Domain: signal sequence (fragment) #status predicted <SIG>  
F:23-236/Product: exotoxin type A (fragment) #status predicted <MAT>  
  
Query Match 87.5%; Score 63; DB 2; Length 236;  
Best Local Similarity 83.3%; Pred. No. 0.00078;  
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
Oy 1 CMYGVTEHEGN 12  
1:||||| ||||  
Db 120 CTVGVTHNEGN 131  
  
RESULT 8  
S18783  
exotoxin type A precursor (allele 3) - Streptococcus pyogenes phage (strain MGAS158 1  
N:Alternate names: scarlet fever toxin  
C:Species: Streptococcus pyogenes phage  
A:Variety: strain MGAS158 isolate Nebraska; strain MGAS485 isolate Yugoslavia; strain  
C:Date: 29-Jan-1993 #sequence\_revision 29-Jan-1993 #text\_change 16-Jul-1999  
R:Accession: S18783; S18793; S18794; S18801; S18798  
R:Nelson, K.; Schlievert, P.M.; Seldner, R.K.; Musser, J.M.  
J. Exp. Med. 174, 1271-1274, 1991  
A:Title: Characterization and clonal distribution of four alleles of the speA gene en  
A:Reference number: S18782; MUID:92044323  
A:Accession: S18783  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-236 <NEU>  
A:Cross-references: EMBL:X61568; NID:q47289; PIDN:CAA43766.1; PID:q47290  
A:Experimental source: strain MGAS158 isolate Nebraska unassigned phage  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199  
A:Accession: S18793  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-236 <NEU>  
A:Cross-references: EMBL:X61569; NID:q47313; PIDN:CAA43767.1; PID:q47314  
A:Experimental source: strain MGAS485 isolate Yugoslavia unassigned phage  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199  
A:Accession: S18794  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-236 <NEU>  
A:Cross-references: EMBL:X61570; NID:q47315; PIDN:CAA43768.1; PID:q47316  
A:Experimental source: strain MGAS491 isolate United Kingdom unassigned phage  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199

A:Accession: S18801  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-236 <NE>  
A:Cross-references: EMBL:X61572; NID:g47333; PIDN:CAA43770.1; PID:g47334  
A:Experimental source: strain MGA5624 isolate Germany unassigned phage  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991  
A:Accession: S18798  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-236 <NE>  
A:Cross-references: EMBL:X61571; NID:g47323; PIDN:CAA43769.1; PID:g47324  
A:Experimental source: strain MGA5495 isolate Germany unassigned phage  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991  
C:Genetics:  
A:Gene: speA3  
C:Superfamily: enterotoxin B  
C:Keywords: exotoxin  
F:1.2/Domain: signal sequence (fragment) #status predicted <SIG>  
F:23-236/Product: exotoxin type A (fragment) #status predicted <MAT>

Query Match 87.5%; Score 63; DB 2; Length 236;  
Best Local Similarity 83.3%; Pred. No. 0.00078;  
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGVTEHNGN 12  
I:|||||  
Db 120 CTVGVTHNGN 131

RESULT 9  
S29659  
exotoxin type A precursor (allele 1) - Streptococcus pyogenes phage T12  
N:Alternate names: erythrogenic toxin; scarlet fever toxin  
C:Species: Streptococcus pyogenes phage T12  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: S29659; S18782; S18784; S18785; S18791; S18796; S18797; S18800  
R:Weeks, C.R.; Ferretti, J.J.  
Infect. Immun. 52, 144-150, 1986  
A:Title: Nucleotide sequence of the type A streptococcal exotoxin (erythrogenic toxin) g  
A:Reference number: S29659; MUID:86166804  
A:Accession: S29659  
A:Molecule type: DNA  
A:Residues: 1-251 <NE>  
A:Cross-references: GB:U04053; EMBL:M19350; NID:g1877426; PIDN:AAC48868.1; PID:g1877430  
J:Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.  
J. Exp. Med. 174, 1271-1274, 1991  
A:Title: Characterization and clonal distribution of four alleles of the speA gene encod  
A:Reference number: S18782; MUID:92044323  
A:Accession: S18782  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 9-244 <NE>  
A:Cross-references: EMBL:X61560; NID:g47287; PIDN:CAA43758.1; PID:g47288  
A:Experimental source: Streptococcus pyogenes strain MGA5156 isolate Nebraska unassigned  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991  
A:Accession: S18784  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 9-244 <NE>  
A:Cross-references: EMBL:X61556; NID:g47291; PIDN:CAA43754.1; PID:g47292  
A:Experimental source: Streptococcus pyogenes strain MGA5165 isolate Minnesota unassigned  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991  
A:Accession: S18785  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 9-244 <NE>  
A:Cross-references: EMBL:X61559; NID:g47293; PIDN:CAA43757.1; PID:g47294  
A:Experimental source: Streptococcus pyogenes strain MGA5167 isolate Texas unassigned ph  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991  
A:Accession: S18791  
A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA  
A:Residues: 9-244 <NE>  
A:Cross-references: EMBL:X61555; NID:g47309; PIDN:CAA43753.1; PID:g47310  
A:Experimental source: Streptococcus pyogenes strain MGA5327 isolate Arizona unassigned  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991  
A:Accession: S18796  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 9-244 <NE>  
A:Cross-references: EMBL:X61557; NID:g47319; PIDN:CAA43755.1; PID:g47320  
A:Experimental source: Streptococcus pyogenes strain MGA5493 isolate France unassigned  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991  
A:Accession: S18797  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 9-244 <NE>  
A:Cross-references: EMBL:X61558; NID:g47321; PIDN:CAA43756.1; PID:g47322  
A:Experimental source: Streptococcus pyogenes strain MGA5494 isolate France unassigned  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991  
A:Accession: S18800  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 9-228 <NE>  
A:Cross-references: EMBL:X61554; NID:g47327; PIDN:CAA43752.1; PID:g47328  
A:Experimental source: Streptococcus pyogenes strain MGA5500 isolate New Zealand unassigned  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991  
C:Genetics:  
A:Gene: speA  
C:Superfamily: enterotoxin B  
C:Keywords: exotoxin  
F:1.30/Domain: signal sequence #status predicted <SIG>  
F:31-251/Product: exotoxin type A #status predicted <MAT>

Query Match 87.5%; Score 63; DB 1; Length 251;  
Best Local Similarity 83.3%; Pred. No. 0.00083;  
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGVTEHNGN 12  
I:|||||  
Db 128 CTVGVTHNGN 139

RESULT 10  
A33953  
enterotoxin D precursor - Staphylococcus aureus  
C:Species: Staphylococcus aureus  
C:Date: 09-Mar-1990 #sequence\_revision 09-Mar-1990 #text\_change 15-Oct-1999  
C:Accession: A33953  
R:Bayles, R.W.; Iandolo, J.J.  
J. Bacteriol. 171, 4799-4806, 1989  
A:Title: Genetic and molecular analyses of the gene encoding staphylococcal enterotox  
A:Reference number: A33953; MUID:89355112  
A:Accession: A33953  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-258 <BAV>  
A:Cross-references: GB:M28521; NID:g1492109; PIDN:AA06195.1; PID:g758691  
C:Superfamily: enterotoxin B

Query Match 83.3%; Score 60; DB 2; Length 258;  
Best Local Similarity 83.3%; Pred. No. 0.0029;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CMYGVTEHNGN 12  
I:|||||  
Db 131 CTVGVTHNGN 142

RESULT 11  
A28664  
enterotoxin A precursor - Staphylococcus aureus

C:Species: Staphylococcus aureus  
 C:Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 15-Oct-1999  
 C:Accession: A28664; A29566  
 R:Betley, M.J.; Mekalanos, J.J.  
 J: Bacteriol. 170, 34-41, 1988  
 A:Title: Nucleotide sequence of the type A staphylococcal enterotoxin gene.  
 A:Reference number: A28664; MUID:88086892  
 A:Accession: A28664  
 A:Molecule type: DNA  
 A:Residues: 1-257 <BET>  
 A:Cross-references: GB:M18970; NID:9153120; PIDN:AAA2661.1; PID:9153121  
 A:Experimental source: strain FR1337  
 R:Huang, I.Y.; Hughes, J.L.; Bergdoll, M.S.; Schantz, E.J.  
 J: Biol. Chem. 262, 7006-7013, 1987  
 A:Title: Complete amino acid sequence of staphylococcal enterotoxin A.  
 A:Reference number: A29566; MUID:87222293  
 A:Accession: A29566  
 A:Molecule type: protein  
 A:Residues: 25-241, 'S', 243-257 <HUA>  
 C:Genetics:  
 A:Gene: entA  
 A:Map position: 6  
 C:Superfamily: enterotoxin B

Query Match 76.4%; Score 55; DB 2; Length 257;  
 Best Local Similarity 75.0%; Pred. No. 0.023;  
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 CMYGGVTEHGN 12  
 ||||| |  
 Db 130 CMYGGVTLHDNN 141

RESULT 12  
 A28179  
 enterotoxin E precursor - Staphylococcus aureus  
 C:Species: Staphylococcus aureus  
 C:Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 15-Oct-1999  
 C:Accession: A28179  
 R:Couch, J.L.; Solitis, M.T.; Betley, M.J.  
 J: Bacteriol. 170, 2954-2960, 1988  
 A:Title: Cloning and nucleotide sequence of the type E staphylococcal enterotoxin gene.  
 A:Reference number: A28179; MUID:88257005  
 A:Accession: A28179  
 A:Molecule type: DNA  
 A:Residues: 1-257 <COU>  
 A:Cross-references: GB:M21319; NID:9153001; PIDN:AAA2661.1; PID:9153002  
 C:Superfamily: enterotoxin B

Query Match 76.4%; Score 55; DB 2; Length 257;  
 Best Local Similarity 75.0%; Pred. No. 0.023;  
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 CMYGGVTEHGN 12  
 ||||| |  
 Db 130 CMYGGVTLHDNN 141

RESULT 13  
 B48826  
 high chorolytic hatching proteinase (EC 3.4.24.-) HCE23 precursor - Japanese medaka  
 C:Species: Oryzias latipes (Japanese medaka)  
 C:Date: 01-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 21-Jul-2000  
 C:Accession: B48826  
 R:Yasumatsu, S.; Yamada, K.; Mitsunaga, K.; Iuchi, I.; Shimada, H.; Yamagami, Dev. Biol. 153, 250-258, 1992  
 A:Title: Isolation of cDNAs for LCE and HCE, two constituent proteases of the hatching  
 A:Reference number: A48826; MUID:93012471  
 A:Accession: B48826  
 A:Molecule type: mRNA  
 A:Residues: 1-270 <YAS>

A:Cross-references: GB:M96170; NID:9213501; PIDN:AAA49438.1; PID:9213502  
 A:Experimental source: orange red variety, embryo  
 A:Note: sequence extracted from NCBI backbone (NCBIN:114769, NCBI:114770)  
 A:Note: part of this sequence, including the amino end of the mature protein, was det  
 C:Superfamily: astacin; astacin homology  
 C:Keywords: glycoprotein; hydrolase; metalloproteinase; zinc  
 F:1-20/Domains: signal sequence #status predicted <STO>  
 F:21-70/Domains: propeptide #status predicted <PRO>  
 F:71-270/Product: low chorolytic hatching proteinase #status predicted <MAT>  
 F:88-270/Domains: astacin homology <AST>  
 F:53/Binding site: carboxylate (Asn) (covalent) #status predicted  
 F:169,173,179,225/Binding site: zinc (His, His, Tyr) #status predicted  
 F:170/Active site: Glu #status predicted

Query Match 63.9%; Score 46; DB 2; Length 270;  
 Best Local Similarity 58.3%; Pred. No. 1;  
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 CMYGGVTEHGN 12  
 ||| |  
 Db 161 CMYGGIIGHHLN 172

RESULT 14  
 C48826  
 high chorolytic hatching proteinase (EC 3.4.24.-) HCE21 precursor - Japanese medaka  
 C:Species: Oryzias latipes (Japanese medaka)  
 C:Date: 08-Feb-1996 #sequence\_revision 08-Feb-1996 #text\_change 03-Dec-1999  
 C:Accession: C48826  
 R:Yasumatsu, S.; Yamada, K.; Akasaka, K.; Mitsunaga, K.; Iuchi, I.; Shimada, H.; Yamagami, Dev. Biol. 153, 250-258, 1992  
 A:Title: Isolation of cDNAs for LCE and HCE, two constituent proteases of the hatchin  
 A:Reference number: A48826; MUID:93012471  
 A:Accession: C48826  
 A:Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-279 <YAS>  
 A:Cross-references: GB:M96171  
 C:Superfamily: astacin; astacin homology  
 C:Keywords: glycoprotein; hydrolase; metalloproteinase; zinc  
 F:1-20/Domains: signal sequence #status predicted <STO>  
 F:21-79/Domains: propeptide #status predicted <PRO>  
 F:80-279/Product: low chorolytic hatching proteinase #status predicted <MAT>  
 F:97-279/Domains: astacin homology <AST>  
 F:62/Binding site: carboxylate (Asn) (covalent) #status predicted  
 F:178,182,188,234/Binding site: zinc (His, His, Tyr) #status predicted  
 F:179/Active site: Glu #status predicted

Query Match 63.9%; Score 46; DB 2; Length 279;  
 Best Local Similarity 58.3%; Pred. No. 1.1;  
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 CMYGGVTEHGN 12  
 ||| |  
 Db 170 CMYGGIIGHHLN 181

RESULT 15  
 T25259  
 hypothetical protein T25B9.2 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 31-Jan-2000  
 C:Accession: T25259  
 R:Matthews, P.  
 submitted to the EMBL Data Library, March 1996  
 A:Reference number: Z20006  
 A:Accession: T25259  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-366 <MIL>  
 A:Cross-references: EMBL:Z70311; PIDN:CAA94374.1; GSPDB:GN00022; CESP:T25B9.2

A;Experimental source: clone T25B9

C;Genetics:

A;Gene: CESP:T25B9.2

A;Map position: 4

A;Intons: 66/3; 171/2; 239/3; 333/1

C;Superfamily: phosphoprotein phosphatase; phosphoesterase core homology; phosphoprotein

Query Match

62.5%; Score 45; DB 2; Length 366;

Best Local Similarity 66.7%; Pred. No. 2.1;

Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CMGCVTEH 9

||:|||||

Db 199 CMHGISSEH 207

Search completed: January 2, 2002, 20:49:24  
Job time: 784 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 2, 2002, 20:46:45 ; Search time 37.4 seconds

(without alignments)  
11.764 Million cell updates/sec

Title: US-09-335-581a-3  
Perfect score: 72  
Sequence: 1 CMYGVTEHEGN 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues  
Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SWISSPROT\_39:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	67	93.1	266	1 ETC1_STAUV	P01553 staphylococ
2	67	93.1	266	1 ETC2_STAUV	P34071 staphylococ
3	67	93.1	266	1 ETC3_STAUV	P23313 staphylococ
4	67	93.1	266	1 ETCB_STAUV	P01552 staphylococ
5	63	87.5	251	1 SPEA_STRPY	P08095 streptococ
6	60	83.3	258	1 ETCX_STAUV	P20723 staphylococ
7	55	76.4	257	1 ETCX_STAUV	P13163 staphylococ
8	55	76.4	257	1 ETCX_STAUV	P12993 staphylococ
9	46	63.9	270	1 HCE1_ORYLA	P31580 oryzias lat
10	46	63.9	279	1 HCE2_ORYLA	P31581 oryzias lat
11	41	56.9	150	1 VCCA_BACD3	P55815 bacillus ps
12	40	55.6	303	1 ROC_HUMAN	P07910 homo sapien
13	40	55.6	455	1 VSDI_CAEBL	P48459 caenorhabdi
14	40	55.6	739	1 VGIQ_ECOLI	O46861 escherichia
15	40	55.6	877	1 AGLU_HORVU	O43763 hordeum vul
16	38	52.8	170	1 RS7_DESMO	P41206 desulfuroc
17	38	52.8	242	1 Z37A_HUMAN	P17032 homo sapien
18	38	52.8	437	1 ERRI_YEAST	P42222 saccharomyc
19	38	52.8	472	1 REI6_SCHPO	P40379 schizosacch
20	37	51.4	310	1 ASTL_COTJA	P46662 coturnix co
21	37	51.4	402	1 NK2R_CAVPO	O64077 cavia porce
22	37	51.4	413	1 HEMO_MANSE	P13398 manduca sex
23	37	51.4	466	1 SRM_MOUSE	O62270 mus musculu
24	37	51.4	523	1 DBP3_YEAST	P20447 saccharomyc
25	37	51.4	969	1 KBF1_HUMAN	P19838 homo sapien
26	37	51.4	971	1 KBF1_MOUSE	P25799 mus musculu
27	37	51.4	3635	1 LMA5_MOUSE	O61001 mus musculu
28	36.5	50.7	463	1 FTBB_CHICK	O02020 gallus gall
29	36	50.0	145	1 MOAE_HELPJ	O95144 heliobacte
30	36	50.0	169	1 PLMN_RAT	O01177 rattus norv
31	36	50.0	234	1 YP24_METTE	P25576 methanobact
32	36	50.0	237	1 YPVA_METTE	P25575 methanobact
33	36	50.0	474	1 MEC3_YEAST	O02574 saccharomyc

34	36	50.0	775	1 TNP3_MOUSE	O60769 mus musculu
35	36	50.0	841	1 SECA_BACSU	P28366 bacillus su
36	36	50.0	842	1 IF2_TREPA	O83861 treponema p
37	36	50.0	908	1 CUC2_MOUSE	O37081 mus musculu
38	36	50.0	918	1 SCRA_LIMPO	O25390 limulus pol
39	36	50.0	1085	1 RBP2_BOVIN	P48820 bos taurus
40	36	50.0	1328	1 AGRI_DISOM	O90404 discopyge o
41	36	50.0	1955	1 AGRI_CHICK	P31696 gallus gall
42	36	50.0	3224	1 RBP2_HUMAN	P49792 homo sapien
43	35.5	49.3	1134	1 TIE1_MOUSE	O06806 mus musculu
44	35.5	49.3	1138	1 TIE1_HUMAN	P35590 homo sapien
45	35	48.6	134	1 YP6_MYCTU	O50625 mycobacteri

## ALIGNMENTS

RESULT 1	ID	ETC1_STAUV	STANDARD:	PRT:	266 AA.
AC	P01553:	ETC1_STAUV			
DT	21-JUL-1986	(Rel. 01, Created)			
DT	01-JAN-1990	(Rel. 13, Last sequence update)			
DT	15-JUL-1999	(Rel. 38, Last annotation update)			
DE	ENTEROTOXIN TYPE C-1 PRECURSOR (SEC1).				
CN	ETC1.				
OS	Staphylococcus aureus.				
OC	Bacteria; Firmicutes; Bacillus/Clostridium group;				
OC	Bacillus/Staphylococcus group; Staphylococcus.				
OX	NCBI_TaxID=1280;				
NP	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=88038352; PubMed=2823067;				
RA	Bonach G.A., Schlievert P.M.;				
RT	"Nucleotide sequence of the staphylococcal enterotoxin C1 gene and				
RT	relatedness to other pyrogenic toxins.";				
RL	Mol. Gen. Genet. 209:15-20(1987).				
RN	[2]				
RP	SEQUENCE OF 28-266.				
RX	MEDLINE=83213327; PubMed=6189824;				
RA	Schmidt J.J., Spero L.;				
RT	"The complete amino acid sequence of staphylococcal enterotoxin C1.";				
RL	J. Biol. Chem. 258:6300-6306(1983).				
CC	-1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION				
CC	STAPHYLOCOCCAL FOOD POISONING SYNDROME.				
CC	-1- SIMILARITY: THE DIFFERENT S.AUREUS ENTEROTOXINS AND S.PYOGENES				
CC	PYROGENIC EXOTOXINS ARE ALL RELATED.				
CC	-----				
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CC	the European Bioinformatics Institute. There are no restrictions on its				
CC	use by non-profit institutions as long as its content is in no way				
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CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>				
CC	or send an email to <a href="mailto:license@sib-sib.ch">license@sib-sib.ch</a> ).				
CC	-----				
DR	EMBL; X05815; CA29260.1; -				
DR	PIR; A01816; ENSAC1.				
DR	PIR; S06356; S06356.				
DR	HSSP; P34071. 1SER2.				
DR	InterPro; IPR001961; Staph_Strep_toxin.				
DR	Pfam; PF01123; Staph_Strep_toxin; 1.				
DR	PRINTS; PR00379; BACTR_TOXIN.				
DR	PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.				
DR	PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.				
KW	Enterotoxin; Toxin; Signal; Superantigen.				
FT	SIGNAL	1	27		ENTEROTOXIN TYPE C-1.
FT	CHAIN	28	266		
FT	DISULFID	120	137		
FT	CONFLICT	177	177		D -> N (IN REF. 2).
SQ	SEQUENCE	266 AA;	30546 MW;	3A7AB59A8986853B	CRC64;

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Query Match          93.1%; Score 67; DB 1; Length 266;
Best Local Similarity 83.3%; Pred. No. 6.9e-05;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 CMGCVTEHGN 12
    |||||:|||||
DB 137 CMGCVTEHGN 148

RESULT 2
ETC3_STAU
ID ETC3_STAU STANDARD; PRT; 266 AA.
AC P34071;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ENTEROTOXIN TYPE C-2 PRECURSOR (SEC2).
GN ETC2.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
OX NCBI_TaxID=1280;
[1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-66.
RX MEDLINE=89277549; PubMed=2543637;
RA Bonach G.A., Schlievert P.M.;
RT "Conservation of the biologically active portions of staphylococcal
RT enterotoxins C1 and C2."
RL Infect. Immun. 57:2249-2252(1989).
[2]
RN X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=96027099; PubMed=7582894;
RA Papageorgiou A.C., Acharya K.R., Shapiro R., Passalacqua E.F.,
RA Brehm R.D., Tranter H.S.;
RT "Crystal structure of the superantigen enterotoxin C2 from
RT Staphylococcus aureus reveals a zinc-binding site."
RL Structure 3:769-779(1995).
[3]
RN X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
RX MEDLINE=96022987; PubMed=7552730;
RA Swaminathan S., Furey W.F., Jr., Pletcher J., Sax M.;
RT "Residues defining V beta specificity in staphylococcal
RT enterotoxins."
RL Nat. Struct. Biol. 2:680-686(1995).
[4]
RN COMPARISON OF STRUCTURE OF SEA AND SEC2.
RX MEDLINE=9734373; PubMed=9191070;
RA Schad E.M., Papageorgiou A.C., Svensson L.A., Acharya K.R.;
RT "A structural and functional comparison of staphylococcal
RT enterotoxins A and C2 reveals remarkable similarity and
RT dissimilarity."
RL J. Mol. Biol. 269:270-280(1997).
-1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC SIMILARITY: THE DIFFERENT S.AUREUS ENTEROTOXINS AND S.PYOGENES
CC PYROGENIC EXOTOXINS ARE ALL RELATED.
PIR: A60114; A60114.
DR PDB; 1STE; 23-DEC-96.
DR PDB; 1SE2; 08-MAR-96.
DR InterPro: IPR001961; Staph_Strep_toxin.
DR Pfam: PF01123; Staph_Strep_toxin; 1.
DR PRINTS: PR00279; BACTRTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
KW Enterotoxin; Toxin; Signal; Superantigen; Zinc; 3D-structure.
FT CHAIN 1 27
FT SIGNAL 1 27
FT CHAIN 28 266 ENTEROTOXIN TYPE C-2.
FT DISULFID 120 137
FT METAL 36 36 ZINC.
FT METAL 110 110 ZINC.
FT METAL 145 145 ZINC.
FT METAL 149 149 ZINC.
SQ SEQUENCE 266 AA; 30604 MW; 8407FB18536FAC08 CRC64;

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Query Match          93.1%; Score 67; DB 1; Length 266;
Best Local Similarity 83.3%; Pred. No. 6.9e-05;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 CMGCVTEHGN 12
    |||||:|||||
DB 137 CMGCVTEHGN 148

RESULT 3
ETC3_STAU
ID ETC3_STAU STANDARD; PRT; 266 AA.
AC P23313;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ENTEROTOXIN TYPE C-3 PRECURSOR (SEC3).
GN ETC3.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
OX NCBI_TaxID=1280;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90220508; PubMed=2325627;
RA Hoyde C.J., Hackett S.P., Bonach G.A.;
RT "Nucleotide sequence of all three type C staphylococcal
RT sequence comparison of all three type C staphylococcal
RT enterotoxins."
RL Mol. Gen. Genet. 220:329-333(1990).
[2]
RN X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS) OF COMPLEX WITH T-CELL RECEPT.
RX MEDLINE=97064178; PubMed=8906797;
RA Fields B.A., Malschodi E.L., Li H., Ysern X., Stauffer C.V.,
RA Schlievert P.M., Karjalainen K., Mariuzza R.A.;
RT "Crystal structure of a T-cell receptor beta-chain complexed with a
RT superantigen."
RL Nature 384:188-192(1996).
-1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC SIMILARITY: THE DIFFERENT S.AUREUS ENTEROTOXINS AND S.PYOGENES
CC PYROGENIC EXOTOXINS ARE ALL RELATED.
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DR EMBL: X51661; CA35972.1; -.
DR PIR; S11885; S11885.
DR PDB; 1JCK; 12-NOV-97.
DR InterPro: IPR001961; Staph_Strep_toxin.
DR Pfam: PF01123; Staph_Strep_toxin; 1.
DR PRINTS: PR00279; BACTRTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
KW Enterotoxin; Toxin; Signal; Superantigen; 3D-structure.
FT CHAIN 1 27
FT SIGNAL 1 27
FT CHAIN 28 266 ENTEROTOXIN TYPE C-3.
FT DISULFID 120 137 BY SIMILARITY
FT METAL 36 36
SQ SEQUENCE 266 AA; 30671 MW; 5ED8A32D11FCA59 CRC64;

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Query Match          93.1%; Score 67; DB 1; Length 266;
Best Local Similarity 83.3%; Pred. No. 6.9e-05;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 CMGCVTEHGN 12

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Db      137 CMYGGVTEHNGN 148

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RESULT  4
ETXB_STAAU STANDARD; PRT: 266 AA.
AC P01552;
DT 21-JUL-1986 (Rel. 01, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ENTEROTOXIN TYPE B PRECURSOR (SEB).
GN ENTB.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=66168029; PubMed=3957869;
RA Jones C.L., Khan S.A.;
RT "Nucleotide sequence of the enterotoxin B gene from Staphylococcus
RT aureus.";
RN [2]
RP SEQUENCE OF 40-91 FROM N.A.
RX MEDLINE=85298255; PubMed=3898073;
RA Raneill D.M., Jones C.L., Johns M.B., Mussey G.J., Khan S.A.;
RT "Molecular cloning of staphylococcal enterotoxin B gene in
RT Escherichia coli and Staphylococcus aureus.";
RN [3]
RP Proc. Natl. Acad. Sci. U.S.A. 82:5850-5854(1985).
RN [4]
RP SEQUENCE OF 28-266 (S-6).
RX MEDLINE=71007902; PubMed=5470821;
RA Huang I.-Y., Bergdoll M.S.;
RT "The primary structure of staphylococcal enterotoxin B. 3. The
RT cyonogen bromide peptides of reduced and aminoethylated enterotoxin
RT B, and the complete amino acid sequence.";
RN [5]
RX J. Biol. Chem. 245:3518-3525(1970).
RN [6]
RX X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RX MEDLINE=93063291; PubMed=1436058;
RA Swaminathan S., Furey W.F. Jr., Fletcher J., Sax M.;
RT "Crystal structure of staphylococcal enterotoxin B, a superantigen.";
RN [7]
RX Nature 359:801-806(1992).
RN [8]
RX X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF COMPLEX WITH MHC II.
RX MEDLINE=94203282; PubMed=8152483;
RA Jardecky T.S., Brown J.H., Gorga J.C., Stern L.J., Urban R.G.,
RA Chl Y.I., Stauffer C., Strominger J.L., Wiley D.C.;
RT "Three-dimensional structure of a human class II histocompatibility
RT molecule complexed with superantigen.";
RN [9]
RX Nature 368:711-718(1994).
RN [10]
RX X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF COMPLEX WITH TCR.
RX MEDLINE=99096298; PubMed=9881971;
RA Li H., Llera A., Tsuchiya D., Leder L., Ysern X., Schlievert P.M.,
RA Katjalainen K., Mariuzza R.A.;
RT "Three-dimensional structure of the complex between a T cell receptor
RT beta chain and the superantigen staphylococcal enterotoxin B.";
RN [11]
RX Immunity 9:807-816(1998).
RN [12]
RX X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
RX MEDLINE=96181012; PubMed=9514739;
RA Papageorgiou A.C., Tranter H.S., Acharya K.R.;
RT "Crystal structure of microbial superantigen staphylococcal
RT enterotoxin B at 1.5-A resolution: implications for superantigen
RT recognition by MHC class II molecules and T-cell receptors.";
RN [13]
RX J. Mol. Biol. 277:61-79(1998).
RN [14]
RX DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
RN STAPHYLOCOCCAL FOOD POISONING SYNDROME.
RN -1- SIMILARITY: THE DIFFERENT S.AUREUS ENTEROTOXINS AND S.PYOGENES
RN PYROGENIC EXOTOXINS ARE ALL RELATED.

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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL, M1118; AAA86550.1; -.
CC DR PIR; A01815; ENSAB6.
CC DR PIR; S27360; S27360.
CC DR PDB; 1SEB; 20-JUN-96.
CC DR PDB; 2SEB; 28-JAN-98.
CC DR PDB; 3SEB; 27-MAY-98.
CC DR PDB; 1SE3; 16-JUN-97.
CC DR PDB; 1SE4; 15-OCT-97.
CC DR PDB; 1SBB; 04-MAR-99.
CC DR InterPro; IPR001961; Staph_Strep_toxin.
CC DR Pfam; PF01123; Staph_Strep_toxin; 1.
CC DR PRINTS; PR00279; BACTR_TOXIN.
CC DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
CC DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
CC DR Enterotoxin; Toxin; Signal; Superantigen; 3D-structure.
CC FT SIGNAL 1 27
CC FT CHAIN 28 266 ENTEROTOXIN TYPE B.
CC FT DISULFID 120 140
CC FT CONFLICT 56 58
CC FT CONFLICT 69 77 DDN -> NND (IN REF. 3).
CC FT CONFLICT 118 118 DQFLYFDLI -> NEFFDLIL (IN REF. 3).
CC FT CONFLICT 128 130 DIN -> NID (IN REF. 3).
CC FT CONFLICT 133 135 OTD -> ENT (IN REF. 3).
CC FT CONFLICT 149 150 NG -> GN (IN REF. 3).
CC FT CONFLICT 156 156 Y -> YV (IN REF. 3).
CC FT CONFLICT 185 186 D -> EQ (IN REF. 3).
CC FT CONFLICT 233 233 OE -> N (IN REF. 3).
CC FT CONFLICT 246 247 DN -> ND (IN REF. 3).
CC FT SEQUENCE 266 AA; 31436 MW; B6D417F61CF018B0 CMC64;
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CC Query Match 93.18; Score 67; DB 1; Length 266;
CC Best Local Similarity 91.78; Pred. No. 6.9e-05;
CC Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
CC
CC Oy 1 CMYGGVTEHNGN 12
CC |||||||11
CC Db 140 CMYGGVTEHNGN 151
CC
CC RESULT 5
CC SPEA_STRPY STANDARD; PRT: 251 AA.
CC AC P08095;
CC DT 01-AUG-1988 (Rel. 08, Created)
CC DT 01-JAN-1990 (Rel. 13, Last sequence update)
CC DT 30-MAY-2000 (Rel. 39, Last annotation update)
CC DE EXOTOXIN TYPE A PRECURSOR (SCARLET FEVER TOXIN) (ERYTHROGENIC TOXIN)
CC (SFE A).
CC GN SPEA.
CC OS Streptococcus pyogenes.
CC OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
CC Streptococcus.
CC OX NCBI_TaxID=1314;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RX MEDLINE=86166804; PubMed=3514452;
CC RA Weeks C.R., Ferretti J.J.;
CC RT "Nucleotide sequence of the type A streptococcal exotoxin
CC (erythrogenic toxin) gene from Streptococcus pyogenes bacteriophage
CC T12.";
CC RN Infect. Immun. 52:144-150(1986).
CC RN [2]
CC RP SEQUENCE FROM N.A.

```

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RA MEDLINE=86284313; PubMed J. J. Schliesser P. M.; Johnson L. P.; L'italien J. J.; Schliesser P. M.; "Streptococcal pyrogenic exotoxin type A (scarlet fever toxin) is related to Staphylococcus aureus enterotoxin B.;" Mol. Gen. Genet. 203:354-356(1986).
RN (3)
RP X-RAY CRYSTALLOGRAPHY (2.57 ANGSTROMS).
RX MEDLINE=99094887; PubMed=9878045; Papadogiorgou A.C.; Collins C.M.; Gultman D.M.; Kline J.B., O'Brien S.M.; Tranter H.S.; Acharya K.R.; "Structural basis for the recognition of superantigen streptococcal pyrogenic exotoxin A (SpeA) by MHC class II molecules and T-cell receptors.;" EMBO J. 18:9-21(1999).
RL
CC -1- DISEASE: THE STREPTOCOCCAL PYROGENIC TOXINS A, B, AND C ARE THE CAUSATIVE AGENTS OF THE SYMPTOMS ASSOCIATED WITH SCARLET FEVER, HAVE BEEN ASSOCIATED WITH STREPTOCOCCAL TOXIC SHOCK-LIKE DISEASE AND MAY PLAY A ROLE IN THE EARLY EVENTS OF RHEUMATIC FEVER.
CC -1- MISCELLANEOUS: THIS TOXIN SEEMS TO BE CODED BY BACTERIOPHAGE T12.
CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES PYROGENIC EXOTOXINS ARE ALL RELATED.
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CC -----
DR EMBL: U04053; AAC6886.1; -.
DR EMBL: X03929; CAA27368.1; -.
DR PIR: A26152; A26152.
DR PIR: S29659; S29659.
DR PDB: 1B1Z; 24-NOV-99.
DR InterPro: IPR001961; Staph.Strep.toxin.
DR Pfam: PF00279; BACTRLTOXIN.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
KW Toxin; Signal; 3D-structure.
FT SIGNAL 1 30
FT CHAIN 31 251
FT DISULFID 117 128
FT CONFLICT 6 6
FT CONFLICT 17 18
FT CONFLICT 25 35
FT CONFLICT 40 40
FT CONFLICT 43 43
FT CONFLICT 47 59
FT CONFLICT 129 129
FT CONFLICT 165 178
FT SEQUENCE 251 AA; 29246 MW; 54001FE4CCBFC3 CRC64;
SQ
Query Match 87.5%; Score 63; DB 1; Length 251;
Best Local Similarity 83.3%; Pred. No. 0.00034;
Matches 10; Conservative 1; Mismatches 0; Gaps 0;
QY 1 CMYGVTEHGN 12
I:|||||
Db 128 CIYGVTHGN 139
RESULT 6
ETXD_STAU STANDARD; PRT; 258 AA.
AC P20723;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)

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DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE ENTEROTOXIN TYPE D PRECURSOR (SPD).
GN ENTD.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; staphylococcus.
OX NCBI_TaxID=1280;
RN RN
RN RP SEQUENCE FROM N.A.
RX MEDLINE=89359112; PubMed=2549000;
RA Bayles K.W., Moutou R.J.;
RT "Genetic and molecular analyses of the gene encoding staphylococcal
RT enterotoxin D."
RL J. Bacteriol. 171:4799-4806(1989).
[2]
RN RN
RN RP SEQUENCE FROM N.A. AND X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RX RC STRAIN=ATCC 23225;
RX MEDLINE=97151473; PubMed=9003758;
RA Sundstroem M., Abrahamson L., Antonsson P., Mehindate K., Mourad W.,
RA Dohlsten M.;
RT "The crystal structure of staphylococcal enterotoxin type D reveals
RT Zn2+-mediated homodimerization."
RL EMBO J. 15:6832-6840(1996).
CC CC
CC -I- SUBUNIT: HOMODIMER; ZINC-DEPENDENT.
CC -I- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -I- SIMILARITY: THE DIFFERENT S.AUREUS ENTEROTOXINS AND S.PYOGENES
CC PROGENIC EXOTOXINS ARE ALL RELATED.
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CC -----
DR DR EMBL, M28521; AAB06195.1; -.
DR PIR: A33953; A33953.
DR HSSP: P13163; 1SX7.
DR InterPro: IPR001961; staph_Strep_toxin.
DR Pfam: PF01123; staph_Strep_toxin_1.
DR PRINTS: PR00277; BACTRTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR Enterotoxin; Toxin; Signal; Superaantigen; Zinc.
KW SIGNAL 1
KW CHAIN 26 258 ENTEROTOXIN TYPE D.
FT METAL 212 212 ZINC.
FT METAL 250 250 ZINC.
FT METAL 252 252 ZINC.
FT VARIANT 114 114 P -> A (IN STRAIN ATCC 23235).
SQ SEQUENCE 258 AA; 29746 MW; 4E7C6A28BD42597FD CRC64;
Query Match 83.3%; Score 60; DB 1; Length 258;
Best local Similarity 83.3%; Pred. No. 0.0012;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CMGQVTEHEGN 12
ID I I I I I I I I I
Db 131 CTGGVTPHEGN 142
RESULT 7
ETX STAU STANDARD; PRT; 257 AA.
AC P13163;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ENTEROTOXIN TYPE A PRECURSOR (SEA).
EN ENTA.

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OS Staphylococcus aureus.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
 CC Bacillus/Staphylococcus group; Staphylococcus.  
 OX NCBI\_TaxID=1280;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FR137;  
 RX MEDLINE=88086892; PubMed=3335483;  
 RA Bielewicz M.J., Mekalanos J.J.;  
 RT "Nucleotide sequence of the type A staphylococcal enterotoxin gene";  
 RL J. Bacteriol. 170:34-41(1988).  
 RN [2]  
 RP SEQUENCE OF 25-257.  
 RX MEDLINE=87222293; PubMed=3584106;  
 RA Huang I.-Y., Hughes J.L., Bergdoll M.S., Schantz E.J.;  
 RT "Complete amino acid sequence of staphylococcal enterotoxin A";  
 RL J. Biol. Chem. 262:7006-7013(1987).  
 RN [3]  
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).  
 RX MEDLINE=95354648; PubMed=7628431;  
 RA Schad E.M., Zaitseva I., Zaitsev V.N., Dohlsien M., Kalland T.,  
 RT "Crystal structure of the superantigen staphylococcal enterotoxin  
 type A";  
 RL EMBO J. 14:3292-3301(1995).  
 RN [4]  
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).  
 RX MEDLINE=97113025; PubMed=8943278;  
 RA Sundstrom M., Hallen D., Svensson A., Schad E., Dohlsien M.,  
 RT "The co-crystal structure of staphylococcal enterotoxin type A with  
 Zn<sup>2+</sup> at 2.7-A resolution. Implications for major histocompatibility  
 complex class II binding";  
 RL J. Biol. Chem. 271:3212-3226(1996).  
 RN [5]  
 RP 3D-STRUCTURE MODELING.  
 RX MEDLINE=96022987; PubMed=7552730;  
 RA Swaminathan S., Furey W.F. Jr., Pletcher J., Sax M.;  
 RT "Residues defining V beta specificity in staphylococcal  
 enterotoxins";  
 RL Nat. Struct. Biol. 2:680-686(1995).  
 RN [6]  
 RP COMPARISON OF STRUCTURE OF SEA AND SEC2.  
 RX MEDLINE=97334373; PubMed=9191070;  
 RA Schad E.M., Papageorgiou A.C., Svensson L.A., Acharya K.R.;  
 RT "A structural and functional comparison of staphylococcal  
 enterotoxins A and C2 reveals remarkable similarity and  
 dissimilarity";  
 RL J. Mol. Biol. 269:270-280(1997).  
 CC -1- SUBUNIT: MONOMER.  
 CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION  
 STAPHYLOCOCCAL FOOD POISONING SYNDROME.  
 CC -1- MISCELLANEOUS: THIS TOXIN SEEMS TO BE CODED BY A BACTERIOPHAGE.  
 CC -1- SIMILARITY: THE DIFFERENT S.AUREUS ENTEROTOXINS AND S.PYROGENES  
 PROGENIC EXOTOXINS ARE ALL RELATED.  
 CC -----  
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 or send an email to license@isb-sib.ch).  
 CC -----  
 CC EMBL; M18970; AAA26681.1; -  
 DR PIR; A28664; A28664.  
 DR PIR; A29566; A29566.  
 DR PDB; 1ESF; 11-JUL-96.  
 DR PDB; 1SEA; 15-OCT-95.  
 DR PDB; 1SXT; 19-NOV-97.  
 DR InterPro; IPR001961; Staph\_Strep\_toxin.  
 DR Pfam; PF01123; Staph\_Strep\_toxin; 1.  
 DR PRINTS; PR00279; BACTRTOXIN.

DR PROSITE; PS00277; STAPH\_STREP\_TOXIN\_1; 1.  
 DR PROSITE; PS00278; STAPH\_STREP\_TOXIN\_2; 1.  
 KW Enterotoxin; Toxin; Signal; Superantigen; Zinc; 3D-structure.  
 FT SIGNAL 1 24  
 FT CHAIN 25 257 ENTEROTOXIN TYPE A.  
 FT DISULFID 120 130  
 FT METAL 25 25 ZINC.  
 FT METAL 211 211 ZINC.  
 FT METAL 249 249 ZINC.  
 FT METAL 251 251 ZINC.  
 FT CONFLICT 242 242 T -> S (IN REF. 2).  
 SQ SEQUENCE 257 AA; 29669 MW; ADEBFSBCAIF14677 CRC64;  
 Query Match 76.4%; Score 55; DB 1; Length 257;  
 Best Local Similarity 75.0%; Pred. NO. 0.0097;  
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1 CMYGVTEHEGN 12  
 Db 130 CMYGVTLHDNN 141  
 RESULT 8  
 ETYPE STAU STANDARD; PRT: 257 AA.  
 ID ETYPE STAU STANDARD; PRT: 257 AA.  
 AC P12993;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE ENTEROTOXIN TYPE E PRECURSOR (SEE).  
 GN ENTE.  
 OS Staphylococcus aureus.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
 CC Bacillus/Staphylococcus group; Staphylococcus.  
 OX NCBI\_TaxID=1280;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-74.  
 RC STRAIN=MJB265;  
 RX MEDLINE=88257005; PubMed=3384800;  
 RA Couch J.L., Solits M.T., Bielewicz M.J.;  
 RT "Cloning and nucleotide sequence of the type E staphylococcal  
 enterotoxin gene";  
 RL J. Bacteriol. 170:2954-2960(1988).  
 RN [2]  
 RP 3D-STRUCTURE MODELING.  
 RX MEDLINE=96022987; PubMed=7552730;  
 RA Swaminathan S., Furey W.F. Jr., Pletcher J., Sax M.;  
 RT "Residues defining V beta specificity in staphylococcal  
 enterotoxins";  
 RL Nat. Struct. Biol. 2:680-686(1995).  
 CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION  
 STAPHYLOCOCCAL FOOD POISONING SYNDROME.  
 CC -1- SIMILARITY: THE DIFFERENT S.AUREUS ENTEROTOXINS AND S.PYROGENES  
 PROGENIC EXOTOXINS ARE ALL RELATED.  
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 CC -----  
 CC EMBL; M21319; AAA26617.1; -  
 DR PIR; A28179; A28179.  
 DR PDB; 1SEE; 15-OCT-95.  
 DR InterPro; IPR001961; Staph\_Strep\_toxin.  
 DR Pfam; PF01123; Staph\_Strep\_toxin; 1.  
 DR PRINTS; PR00277; STAPH\_STREP\_TOXIN\_1; 1.  
 DR PROSITE; PS00277; STAPH\_STREP\_TOXIN\_1; 1.  
 DR PROSITE; PS00278; STAPH\_STREP\_TOXIN\_2; 1.  
 KW Enterotoxin; Toxin; Signal; Superantigen; 3D-structure.

FT SIGNAL 1 27  
 FT CHAIN 28 257 ENTEROTOXIN TYPE E.  
 SQ SEQUENCE 257 AA; 29358 MM; 27EDA9AB97770CE3 CRC64;

Query Match 76.4%; Score 55; DB 1; Length 257;  
 Best Local Similarity 75.0%; Pred. No. 0.0097;  
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 CMYGVTEHSGN 12  
 DB 130 CMYGVTLHDNN 141

RESULT 9  
 HCEL ORYLA STANDARD; PRT: 270 AA.  
 AC P31580;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE HIGH CHORIOLYTIC ENZYME 1 PRECURSOR (EC 3.4.24.67) (HATCHING ENZYME  
 ZINC-PROTEASE HCE 1 SUBUNIT) (CHORIOLYSIN H 1).  
 GN HCE 23.  
 OS Oryzias latipes (Medaka fish).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;  
 OC Belontiiformes; Adriantichthyidae; Oryziinae; Oryzias.  
 OX NCBI\_TaxID=8090;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 71-119 AND 208-223.  
 RC TISSUE=Embryo;  
 RX MEDLINE=93012471; PubMed=1397682;  
 RA Yasumasa S., Yamada K., Akasaka K., Mitsuura K., Iuchi I.,  
 RA Shimada H., Yamagami K.;  
 RT \*Isolation of cDNAs for LCE and HCE, two constituent proteases of the  
 RT hatching enzyme of Oryzias latipes, and concurrent expression of the  
 RT their mRNAs during development.\*;  
 RL Dev. Biol. 153:250-258(1992).  
 CC -1- FUNCTION: PARTICIPATES IN THE BREAKDOWN OF THE EGG ENVELOPE,  
 CC WHICH IS DERIVED FROM THE EGG EXTRACELLULAR MATRIX, AT THE TIME  
 CC OF HATCHING. THUS ALLOWING THE NEWLY HATCHED FISH TO SWIM FREE.  
 CC HCE BINDS TIGHTLY TO THE EGG ENVELOPE WHILE IT EXERTS THE  
 CC CHORIOLYTIC SMELLING ACTION.  
 CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF THE INNER LAYER OF FISH EGG  
 CC ENVELOPE. ALSO HYDROLYSES CASEIN AND SMALL MOLECULE SUBSTRATES  
 CC SUCH AS SUC-LEU-LEU-VAL-TYR-|-MCA.  
 CC -1- COFACTOR: BINDS ONE ZINC ION.  
 CC -1- SUBCELLULAR LOCATION: STORED AS PROENZYMES IN THE ZYMOGEN  
 CC GRANULES.  
 CC -1- DEVELOPMENTAL STAGE: PRODUCTION OF THE PROTEIN STARTS IN DAY  
 CC 2 TO DAY 3 EMBRYOS AND INCREASES THEREAFTER UNTIL HATCHING.  
 CC -1- PTM: O-GLYCOSYLATED (PROBABLE).  
 CC -1- MISCELLANEOUS: IN MEDAKA THE HATCHING ENZYME SYSTEM IS COMPOSED OF  
 CC TWO DISTINCT PROTEASES, THE HIGH CHORIOLYTIC ENZYME (HCE), OF  
 CC WHICH THERE ARE TWO ISOFORMS, AND THE LOW CHORIOLYTIC ENZYME  
 CC (LCE).  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A (ZINC  
 CC METALLOPROTEASE); ALSO KNOWN AS THE ASPACIN SUBFAMILY.  
 CC  
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 CC  
 CC EMBL: M96170; AAA43438.1; -  
 CC DR PIR: B48826; B48826.  
 CC DR HSSP: P07584; 11AD.  
 CC DR MEROPS: M12.007; -.

DR InterPro: IPR001506; Astacin.  
 DR InterPro: IPR000130; Zn\_Mrpeptidse.  
 DR Pfam: PF01400; Astacin. 1.  
 DR PRINTS: PR00480; ASTACIN.  
 DR SMART: SM00235; zmc. 1.  
 DR PROSITE: PS00142; ZINC-PROTEASE; 1.  
 DR Hydrolyase; Metalloprotease; Zinc; Glycoprotein; Zymogen; Signal.  
 FT SIGNAL 1 20  
 FT PROPEP 21 70 ACTIVATION PEPTIDE.  
 FT CHAIN 71 270 HIGH CHORIOLYTIC ENZYME 1.  
 FT METAL 169 169 ZINC (CATALYTIC) (BY SIMILARITY).  
 FT ACT SITE 170 170 BY SIMILARITY.  
 FT METAL 173 173 ZINC (CATALYTIC) (BY SIMILARITY).  
 FT METAL 179 179 ZINC (CATALYTIC) (BY SIMILARITY).  
 FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 270 AA; 30392 MM; DB5C972906E3735A CRC64;

Query Match 63.9%; Score 46; DB 1; Length 270;  
 Best Local Similarity 58.3%; Pred. No. 0.43;  
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 CMYGVTEHSGN 12  
 DB 161 CMYSGIIQHLEIN 172

RESULT 10  
 HCE2 ORYLA STANDARD; PRT: 279 AA.  
 ID HCE2 ORYLA  
 AC P31581;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE HIGH CHORIOLYTIC ENZYME 2 PRECURSOR (EC 3.4.24.67) (HATCHING ENZYME  
 ZINC-PROTEASE HCE 2 SUBUNIT) (CHORIOLYSIN H 2).  
 GN HCE 21.  
 OS Oryzias latipes (Medaka fish).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;  
 OC Belontiiformes; Adriantichthyidae; Oryziinae; Oryzias.  
 OX NCBI\_TaxID=8090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Embryo;  
 RX MEDLINE=93012471; PubMed=1397682;  
 RA Yasumasa S., Yamada K., Akasaka K., Mitsuura K., Iuchi I.,  
 RA Shimada H., Yamagami K.;  
 RT \*Isolation of cDNAs for LCE and HCE, two constituent proteases of the  
 RT hatching enzyme of Oryzias latipes, and concurrent expression of  
 RT their mRNAs during development.\*;  
 RL Dev. Biol. 153:250-258(1992).  
 CC -1- FUNCTION: PARTICIPATES IN THE BREAKDOWN OF THE EGG ENVELOPE,  
 CC WHICH IS DERIVED FROM THE EGG EXTRACELLULAR MATRIX, AT THE TIME  
 CC OF HATCHING. THUS ALLOWING THE NEWLY HATCHED FISH TO SWIM FREE.  
 CC HCE BINDS TIGHTLY TO THE EGG ENVELOPE WHILE IT EXERTS THE  
 CC CHORIOLYTIC SMELLING ACTION.  
 CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF THE INNER LAYER OF FISH EGG  
 CC ENVELOPE. ALSO HYDROLYSES CASEIN AND SMALL MOLECULE SUBSTRATES  
 CC SUCH AS SUC-LEU-LEU-VAL-TYR-|-MCA.  
 CC -1- COFACTOR: BINDS ONE ZINC ION.  
 CC -1- SUBCELLULAR LOCATION: STORED AS PROENZYMES IN THE ZYMOGEN  
 CC GRANULES.  
 CC -1- DEVELOPMENTAL STAGE: PRODUCTION OF THE PROTEIN STARTS IN DAY  
 CC 2 TO DAY 3 EMBRYOS AND INCREASES THEREAFTER UNTIL HATCHING.  
 CC -1- PTM: O-GLYCOSYLATED (PROBABLE).  
 CC -1- MISCELLANEOUS: IN MEDAKA THE HATCHING ENZYME SYSTEM IS COMPOSED OF  
 CC TWO DISTINCT PROTEASES, THE HIGH CHORIOLYTIC ENZYME (HCE), OF  
 CC WHICH THERE ARE TWO ISOFORMS, AND THE LOW CHORIOLYTIC ENZYME  
 CC (LCE).  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A (ZINC  
 CC METALLOPROTEASE); ALSO KNOWN AS THE ASPACIN SUBFAMILY.  
 CC

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CC -----
DR EMBL; M96171; AAA49439.1; -.
DR HSPD; P07584; 1IAD.
DR MEROPS; M12.007; -.
DR InterPro; IPR001506; Astacin.
DR InterPro; IPR00130; Zn_MTPeptide.
DR Pfam; PF01400; Astacin; 1.
DR PRINTS; PR00480; ASTACIN.
DR SMART; SM00235; zmc; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Hydroxylase; Metalloprotease; Zinc; Glycoprotein; zymogen; Signal.
FT SIGNAL 1 20
FT PROPEP 21 79 ACTIVATION PEPTIDE.
FT CHAIN 80 279 HIGH CHORIOLYTIC ENZYME 2.
FT METAL 178 178 ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT_SITE 179 179 BY SIMILARITY.
FT METAL 182 182 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 188 188 ZINC (CATALYTIC) (BY SIMILARITY).
FT CARBOHYD 62 62 N-LINKED (GLCNAC. . .) (POTENTIAL).
SO SEQUENCE 279 AA; 31490 MW; 00244107A8B01B8C CRC64;
OY 1 CMYGVTEHEGHN 12
Db 170 CMVSGITIOHELN 181
RESULT 11
YCQA_BACP3
ID YCQA_BACP3 STANDARD; PRT; 150 AA.
AC P55815;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HYPOTHEICAL PROTEIN IN CCCA 5'REGION (FRAGMENT).
OS Bacillus PS3 (Thermophilic bacterium PS-3).
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_Taxid=70306;
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE=93379042; PubMed=7916623;
RA Fujiwara Y., Oka M., Hamamoto T., Sone N.;
RT "Cytochrome c-551 of the thermophilic bacterium PS3, DNA sequence and
RT analysis of the mature cytochrome c-551."
RL Blochum. Biophys. Acta 1144:213-219(1993).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -1- SIMILARITY: TO B.SUBTILIS YPDC, YOFU AND YITT.
CC -----
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CC -----
DR EMBL; X63125; -. NOT_ANNOTATED COS.
KW Hypothetical protein; Transmembrane.
FT NON_TER 1 1
FT TRANSMEM 19 39 POTENTIAL.

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SQ SEQUENCE 150 AA; 16394 MW; AEFEB92DB2CF7447 CRC64;

Query Match 56.9%; Score 41; DB 1; Length 150;
Best Local Similarity 87.5%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 YGVTEHE 10
   ||| ||||
Db 99 YGVTEHE 106

RESULT 12
ROC_HUMAN STANDARD; PRT; 303 AA.
AC P07910; P22628;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEINS C1/C2 (HNRP C1 / HNRP C2).
GN HNRP C.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
CX NCBI;taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=90099350; Pubmed=2557628;
RX Bird C.G., Swanson M.S., Goerlach M., Dreyfuss G.;
RT "Primary structures of the heterogeneous nuclear ribonucleoprotein
RT A2, B1, and C2 proteins: a diversity of RNA binding proteins is
RT generated by small peptide inserts."
RL Proc. Natl. Acad. Sci. U.S.A. 86:9788-9792(1989).
RN [2]
RP SEQUENCE OF 1-107 AND 121-303 FROM N.A.
RX MEDLINE=87257872; Pubmed=3110598;
RA Swanson M.S., Nakagawa T.Y., Levan K., Dreyfuss G.;
RT "Primary structure of human nuclear ribonucleoprotein particle C
RT proteins: conservation of sequence and domain structures in
RT heterogeneous nuclear RNA, mRNA, and pre-rRNA-binding proteins."
RL Mol. Cell. Biol. 7:1731-1739(1987).
RN [3]
RP PARTIAL SEQUENCE AND CHARACTERIZATION.
RX MEDLINE=90067819; Pubmed=2587210;
RA Merrill B.M., Barnett S.F., Lestougeon W.M., Williams K.R.;
RT "Primary structure differences between proteins C1 and C2 of Hela 40S
RT nuclear ribonucleoprotein particles."
RL Nucleic Acids Res. 17:8441-8449(1989).
RN [4]
RP STRUCTURE BY NMR OF 1-94.
RX MEDLINE=92329450; Pubmed=1385725;
RA Witekleng M., Goerlach M., Friedlachs M., Dreyfuss G., Mueller L.;
RT "H. 13C and 15N NMR assignments and global folding pattern of the
RT RNA-binding domain of the human hnRNP C proteins."
RL Biochemistry 31:6254-6265(1992).
RN [5]
RP STRUCTURE BY NMR OF 1-94.
RX MEDLINE=92371436; Pubmed=1380452;
RA Goerlach M., Witekleng M., Beckman R.A., Mueller L., Dreyfuss G.;
RT "Interaction of the RNA-binding domain of the hnRNP C proteins with
RT RNA."
RL EMBO J. 11:3289-3295(1992).
CC -1- FUNCTION: MAY PLAY A ROLE IN RIBONUCLEOSOME ASSEMBLY BY
CC NEUTRALIZING BASIC PROTEINS SUCH AS A AND B CORE HNRP.
CC -1- SUBCELLULAR LOCATION: NUCLEAR; COMPONENT OF RIBONUCLEOSOMES.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: C1 AND C2 (SHOWN HERE); ARE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC -1- PM: PHOSPHORYLATED (PROBABLE).
CC -1- SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).
CC -----
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 CC -----  
 DR EMBL: M29063; AAA3576.1; -  
 DR EMBL: M16342; AAA52680.1; -  
 DR PIR: G34504; C34504.  
 DR PIR: A26885; A26885.  
 DR SWISS-2DPAGE: P07910; HUMAN.  
 DR Aarhus/Ghent-2DPAGE: 7207; IEF.  
 DR Aarhus/Ghent-2DPAGE: 7222; IEF.  
 DR MIM: 164020;  
 DR InterPro: IPR000504; RRM.  
 DR Pfam: PF00076; rrm; 1.  
 DR SMART: SM00360; RRM; 1.  
 DR PROSITE: PS50102; RRM; 1.  
 DR PROSITE: PS00030; RRM\_RNP\_1; 1.  
 DR Nuclear protein; RNA-binding; Ribonucleoprotein; Phosphorylation;  
 KW Alternative splicing.  
 FT DOMAIN 16 87 RNA-BINDING (RRM).  
 FT DOMAIN 155 161 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
 FT DOMAIN 181 303 ASP/GLU-RICH (ACIDIC).  
 FT VARSPLIC 108 120 MISSING (IN ISOPFORM HNRNP C1).  
 SO SEQUENCE 303 AA; 33298 MW; E1B08298184AAC46 CRC64;

Query Match 55.6%; Score 40; DB 1; Length 303;  
 Best Local Similarity 87.5%; Pred. No. 5.8;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 MYGVTEH 9  
 Db 104 MYGVTEH 111

RESULT 13  
 YSD1\_CAEEL STANDARD; PRT; 455 AA.  
 AC P48459;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 01-FEB-1996 (Rel. 33, Last annotation update)  
 DE PUTATIVE SERINE/THREONINE PROTEIN PHOSPHATASE C23G10.1 IN CHROMOSOME  
 DE II (RC 3.1.3.16).  
 GN C23G10.1.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;  
 OC Rhabditidae; Pelodierinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RA Latreille P.;  
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases  
 CC -1- CATALYTIC ACTIVITY: A PHOSPHOPROTEIN + H<sub>2</sub>O = A PROTEIN +  
 CC ORTHOPHOSPHATE (THIS ENZYME IS SERINE/THREONINE SPECIFIC).  
 CC -1- SIMILARITY: BELONGS TO THE PPP FAMILY OF PHOSPHATASES. PP-1  
 CC SUBFAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: U39851; AAA81073.1; -  
 DR HSSP: P08129; 1F7M.  
 DR Wormpep: C23G10.1; CE01808.  
 DR InterPro: IPR000934; Ser\_thr\_phosphatse.  
 DR InterPro: IPR001394; UCH-2.

DR Pfam: PF00149; STphosphatase; 1.  
 DR Pfam: PF00442; UCH-1; 1.  
 DR PRINTS: PR00114; STPHPTASE.  
 DR SMART: SM00156; PP2Ac; 1.  
 DR PROSITE: PS00125; SER\_THR\_PHOSPHATASE; 1.  
 KW Hypothetical protein; Hydrolase; Iron; Manganese.  
 FT METAL 191 191 IRON (BY SIMILARITY).  
 FT METAL 193 193 IRON (BY SIMILARITY).  
 FT METAL 221 221 IRON AND MANGANESE (BY SIMILARITY).  
 FT METAL 253 253 MANGANESE (BY SIMILARITY).  
 FT ACT\_SITE 254 254 GENERAL ACID (BY SIMILARITY).  
 FT METAL 305 305 MANGANESE (BY SIMILARITY).  
 FT METAL 379 379 MANGANESE (BY SIMILARITY).  
 SO SEQUENCE 455 AA; 51837 MW; BEB5A1A94FFEBB CRC64;

Query Match 55.6%; Score 40; DB 1; Length 455;  
 Best Local Similarity 87.5%; Pred. No. 8.7;  
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 CMVGVTEH 9  
 Db 303 CMVGVTEH 311

RESULT 14  
 YGIO\_ECOLI STANDARD; PRT; 739 AA.  
 AC Q46861; Q46862;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 20-AUG-2001 (Rel. 40, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE HYPOTHETICAL 83.5 KDA PROTEIN IN METC-SUP1 INTERGENIC REGION.  
 GN YGIO OR B3015/B3016.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Escherichia.  
 OX NCBI\_TaxID=562;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-K12 / MG1655;  
 RX MEDLINE=9742617; PubMed=9278503;  
 RA Blatner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
 RA Mau B., Shao Y.;  
 RT "The complete genome sequence of Escherichia coli K-12";  
 RL Science 277:1453-1474(1997).  
 RN (2)  
 RP CONCEPTUAL TRANSLATION.  
 RC Rudd K.E.;  
 RL Unpublished observations (JUN-1999).  
 CC -1- SIMILARITY: TO M.JANASCHIT M01155. ALSO SOME SIMILARITY TO FAMILY  
 CC UPF0004.  
 CC -1- CAUTION: THIS IS A CONCEPTUAL TRANSLATION; A FRAMESHIFT WAS  
 CC INTRODUCED IN POSITION 319 TO PRODUCE THIS ORF.  
 CC -----  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch))  
 CC -----  
 DR EMBL: U28377; AAA69183.1; ALT\_FRAME.  
 DR EMBL: U28377; AAA69184.1; ALT\_FRAME.  
 DR EMBL: AE000383; AAC76052.1; ALT\_FRAME.  
 DR EMBL: AE000383; AAC76051.1; ALT\_FRAME.  
 DR Ecocore: EG13019; YGIO.  
 KW Hypothetical protein; Complete proteome.  
 SO SEQUENCE 739 AA; 83503 MW; ECE565EC8915384A CRC64;

Query Match 55.68; Score 40; DB 1; Length 729;  
 Best Local Similarity 54.58; Pred. No. 14;  
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 CMYGVTEHEG 11  
 1:|||||  
 DB 390 CSFCSITEHEG 400

|||||:1  
 DB 481 YGVTEYE 488

Search completed: January 2, 2002, 20:50:15  
 Job time: 210 sec

RESULT 15  
 ID AGLU\_HORVU STANDARD; PRT; 877 AA.  
 AC 043763;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE ALPHA-GLUCOSIDASE PRECURSOR (EC 3.2.1.20) (MALTASE).  
 OS Hordeum vulgare (Barley).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Trilicaceae; Hordeum.  
 OX NCBI\_TaxID=4513;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. MOREX; TISSUE=Aleucone;  
 RX MEDLINE=96178863; PubMed=9616248;  
 RA Tibbot B.K., Skadsen R.W.;  
 RT "Molecular cloning and characterization of a gibberellin-inducible,  
 RT putative alpha-glucosidase gene from barley."  
 RL Plant Mol. Biol. 30:229-241(1996).  
 CC -1 CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL, NON-REDUCING  
 CC 1,4-LINKED D-GLUCOSE RESIDUES WITH RELEASE OF D-GLUCOSE.  
 CC -1 TISSUE SPECIFICITY: HIGH LEVELS SEEN IN THE ALEURONE AND SCUTELLUM  
 CC AFTER GERMINATION, WHILE LOW LEVELS ARE FOUND IN DEVELOPING SEEDS.  
 CC -1 DEVELOPMENTAL STAGE: LEVELS INCREASE STEADILY THROUGHOUT  
 CC IMBIBITION REACHING MAXIMUM LEVELS AT DAY 7. DURING GERMINATION,  
 CC LEVELS INCREASE FROM DAY 2, REACH MAXIMUM LEVELS AT DAY 3 AND  
 CC DECLINE AFTER DAY 5.  
 CC -1 INDUCTION: BY GIBBERELLIN A3 (GA).  
 CC -1 SIMILARITY: BELONGS TO FAMILY 31 OF GLYCOSYL HYDROLASES.  
 CC -----  
 CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: U22450; AAB02985.1; -  
 DR InterPro: IPR000322; Glyco\_hydro\_31.  
 DR Pfam: PF01055; Glyco\_hydro\_31; 1.  
 DR PROSITE: PS00129; GLYCOSYL\_HYDROL\_F31.1; 1.  
 DR PROSITE: PS00707; GLYCOSYL\_HYDROL\_F31.2; 1.  
 KW Hydrolase; Glycosidase; Glycoprotein; Signal.  
 FT SIGNAL 1 23 POTENTIAL.  
 FT CHAIN 24 877 ALPHA-GLUCOSIDASE.  
 FT ACT\_SITE 437 437 BY SIMILARITY.  
 FT CARBOHYD 191 191 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 298 298 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 391 391 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 471 471 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 570 570 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 877 AA; 96933 MW; E3B5C16E4588C492 CRC64;

Query Match 55.68; Score 40; DB 1; Length 877;  
 Best Local Similarity 87.58; Pred. No. 17;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 YGVTEHE 10





GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 2, 2002, 20:48:15 ; Search time 92.66 Seconds  
(Without alignments)  
18.943 Million cell updates/sec

Title: US-09-335-581a-3  
Perfect score: 72  
Sequence: 1 CMGGVTEHGN 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :  
1: SPTEMBL\_17:\*  
2: sp\_archaea:\*  
3: sp\_bacteria:\*  
4: sp\_fungi:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_protent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	69	95.8	136	2	099T49
2	67	93.1	234	2	09R5X4
3	67	93.1	239	2	005157
4	67	93.1	239	2	053678
5	67	93.1	239	2	006531
6	67	93.1	239	2	006532
7	67	93.1	239	2	006533
8	67	93.1	239	2	006534
9	67	93.1	239	2	006535
10	67	93.1	271	2	09F0L6
11	63	87.5	222	2	09S5Z4
12	63	87.5	222	2	09R931
13	63	87.5	236	2	054696
14	63	87.5	236	2	054779
15	63	87.5	236	2	057453
16	63	87.5	236	2	057453
17	60	83.3	179	2	P97163
18	59	81.9	260	2	054738
19	59	81.9	260	2	054971

20	59	81.9	260	2	054739	054739 streptococ
21	58	80.6	258	2	09EZM4	09EZM4 streptococ
22	58	80.6	268	2	085217	085217 streptococ
23	55	76.4	260	2	099SU3	099SU3 streptococ
24	54	75.0	260	2	099T46	099T46 streptococ
25	54	75.0	261	2	09EZM8	09EZM8 streptococ
26	46	63.9	266	13	013116	013116 oryzias lat
27	45	62.5	366	5	027528	027528 caenorhabd1
28	45	62.5	375	5	09XW33	09XW33 caenorhabd1
29	43	59.7	347	4	09NM14	09NM14 homo sapien
30	43	59.7	1266	4	09NTE6	09NTE6 homo sapien
31	43	59.7	1353	4	09BY58	09BY58 homo sapien
32	42	58.3	203	10	065135	065135 lycopersico
33	41	56.9	366	2	09AAC7	09AAC7 caulobacter
34	41	56.9	644	10	023460	023460 arabidops1s
35	41	56.9	664	10	09ZM29	09ZM29 arabidops1s
36	41	56.9	669	10	09ZM29	09ZM29 arabidops1s
37	41	56.9	690	10	09L1B7	09L1B7 arabidops1s
38	40	55.6	156	2	09ABR6	09ABR6 caulobacter
39	40	55.6	157	2	099P77	099P77 streptococ
40	40	55.6	347	2	09XAN5	09XAN5 streptomyc
41	40	55.6	354	11	09JUS1	09JUS1 mus musculu
42	40	55.6	367	5	09NAP8	09NAP8 caenorhabd1
43	40	55.6	373	11	09QYV1	09QYV1 rattus norv
44	40	55.6	380	4	013086	013086 homo sapien
45	40	55.6	388	10	09STX2	09STX2 arabidops1s

## ALIGNMENTS

RESULT 1  
ID 099T49 PRELIMINARY; PRT; 136 AA.  
AC 099T49;  
DT 01-JUN-2001 (TREMBlrel. 17, Created)  
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
DE ENTEROTOXIN YENT2.  
CN YENT2 OR SA1644.  
OS Staphylococcus aureus subsp. aureus N315.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
OC Bacillus/Staphylococcus group; Staphylococcus.  
OX NCBI\_Taxid=158879;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,  
RA Cui L., Oguchi A., Aoki K.I., Nagai Y., Lian J., Ito T., Kanamori M.,  
RA Matsunaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y.,  
RA Takahashi N.K., Sawano T., Inoue R.I., Kato C., Sekimizu K.,  
RA Hirakawa H., Kohara S., Goto S., Yabuzaki J., Kanehisa M.,  
RA Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M.,  
RA Ogasawara N., Hayashi H., Hiramatsu K.,  
RT "Whole genome sequencing of methicillin-resistant Staphylococcus  
RT aureus."  
RT Lancet 357:1225-1240(2001).  
RL EMBL: AP003135; BAB42912.1; -  
KW Complete Proteome.  
SQ SEQUENCE 136 AA; 15945 MW; D7CB619820C45FE CRC64;

Query Match 95.8%; Score 69; DB 2; Length 136;  
Best Local Similarity 91.7%; Pred. No. 4.7e-05;  
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CMGGVTEHGN 12  
|||||  
Db 5 CMGGVTEHGN 16  
|||||  
RESULT 2  
09R5X4  
ID 09R5X4 PRELIMINARY; PRT; 234 AA.

AC Q095X4;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE ENTEROTOXIN-PYROGENIC TOXIN.  
OS Staphylococcus.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
CC Bacillus/Staphylococcus group.  
OX NCBI\_Taxid=1279;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=9432595; Pubmed=8049778;  
RA Van den Bussche R.A., Lyon J.D., Bohach G.A.;  
RL Mol. Phylogenet. Evol. 2:281-292(1993).  
DR HSSP; P34071; 1SE2.  
DR InterPro; IPR001961; Staph.Strep.toxin.  
DR Pfam; PF01123; Staph.Strep.toxin; 1.  
DR PRINTS; PR00279; BACTRTOXIN.  
DR PROSITE; PS00277; STAPH\_STREP\_TOXIN\_1; 1.  
DR PROSITE; PS00278; STAPH\_STREP\_TOXIN\_2; 1.  
SQ SEQUENCE 234 AA; 27122 MW; D6A7B45FB9810052 CRC64;

Query Match 93.18; Score 67; DB 2; Length 234;  
Best Local Similarity 83.38; Pred. No. 0.00021;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 CMYGVTEHEGN 12  
|||||:|||||  
Db. 105 CMYGGITKHEGN 116

RESULT 3  
005157  
ID- 005157 PRELIMINARY; PRT; 239 AA.  
AC 005157;  
DT 01-JUL-1997 (TREMBLrel. 04, Created)  
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE TYPE C ENTEROTOXIN (FRAGMENT).  
OS Staphylococcus intermedius.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
CC Bacillus/Staphylococcus group; Staphylococcus.  
OX NCBI\_Taxid=1285;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=95-011195;  
RA Edwards V.M., Deringer J.R., Callantine S.D., Dechald C.F.,  
RL Berger P.H., Kapur V., Stauffer C.V., Bohach G.A.;  
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U91526; AAB50246.1; -.  
DR HSSP; P23313; 1JCK.  
DR InterPro; IPR001961; Staph.Strep.toxin.  
DR Pfam; PF01123; Staph.Strep.toxin; 1.  
DR PRINTS; PR00279; BACTRTOXIN.  
DR PROSITE; PS00277; STAPH\_STREP\_TOXIN\_1; 1.  
DR PROSITE; PS00278; STAPH\_STREP\_TOXIN\_2; 1.  
FT NON\_TER 1  
SQ SEQUENCE 239 AA; 27536 MW; D66064460DE4191 CRC64;

Query Match 93.18; Score 67; DB 2; Length 239;  
Best Local Similarity 83.38; Pred. No. 0.00021;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 CMYGVTEHEGN 12  
|||||:|||||  
Db. 110 CMYGGITKHEGN 121

RESULT 4  
053678  
ID Q53678 PRELIMINARY; PRT; 239 AA.

AC Q053678;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE ENTEROTOXIN (FRAGMENT).  
OS Staphylococcus aureus.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
CC Bacillus/Staphylococcus group; Staphylococcus.  
OX NCBI\_Taxid=1280;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94011313; Pubmed=8406814;  
RA Marr J.C., Lyon J.D., Roberson J.R., Luper M., Bohach G.A.;  
RL "Characterization of novel type C staphylococcal enterotoxins:  
RT biological and evolutionary implications.";  
RL Infect. Immun. 61:4254-4262(1993).  
DR EMBL; L13376; AAA26620.1; -.  
DR HSSP; P34071; 1SE2.  
DR InterPro; IPR001961; Staph.Strep.toxin.  
DR Pfam; PF01123; Staph.Strep.toxin; 1.  
DR PRINTS; PR00279; BACTRTOXIN.  
DR PROSITE; PS00277; STAPH\_STREP\_TOXIN\_1; 1.  
DR PROSITE; PS00278; STAPH\_STREP\_TOXIN\_2; 1.  
FT NON\_TER 1  
SQ SEQUENCE 239 AA; 27618 MW; A13E7EB25C6989C2 CRC64;

Query Match 93.18; Score 67; DB 2; Length 239;  
Best Local Similarity 83.38; Pred. No. 0.00021;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 CMYGVTEHEGN 12  
|||||:|||||  
Db. 110 CMYGGITKHEGN 121

RESULT 5  
006531  
ID 006531 PRELIMINARY; PRT; 239 AA.  
AC Q06531;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE ENTEROTOXIN TYPE C-4 (SEC4446) (FRAGMENT).  
OS Staphylococcus aureus.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
CC Bacillus/Staphylococcus group; Staphylococcus.  
OX NCBI\_Taxid=1280;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=4446;  
RX MEDLINE=94011313; Pubmed=8406814;  
RA Marr J.C., Lyon J.D., Roberson J.R., Luper M., Bohach G.A.;  
RL "Characterization of novel type C staphylococcal enterotoxins:  
RT biological and evolutionary implications.";  
RL Infect. Immun. 61:4254-4262(1993).  
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION  
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.  
CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES  
CC PYROGENIC EXOTOXINS ARE ALL RELATED.  
DR EMBL; L13374; AAA26618.1; -.  
DR HSSP; P34071; 1SE2.  
DR InterPro; IPR001961; Staph.Strep.toxin.  
DR Pfam; PF01123; Staph.Strep.toxin; 1.  
DR PRINTS; PR00279; BACTRTOXIN.  
DR PROSITE; PS00277; STAPH\_STREP\_TOXIN\_1; 1.  
DR PROSITE; PS00278; STAPH\_STREP\_TOXIN\_2; 1.  
KW Enterotoxin; Toxin; Superantigen.  
FT NON\_TER 1  
SQ SEQUENCE 239 AA; 27612 MW; BB7BD6204731ED24 CRC64;

Query Match 93.1%; Score 67; DB 2; Length 239;  
Best Local Similarity 83.3%; Pred. No. 0.00021;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 CMYGVTEHGN 12  
DB 110 CMYGVTEHGN 121

RESULT 6  
006532 PRELIMINARY; PRT; 239 AA.

AC 006532;  
DT 01-NOV-1996 (TREMblrel. 01, Created)  
DE 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
DE 01-JUN-2001 (TREMblrel. 17, Last annotation update)  
DE ENTEROTOXIN TYPE C-7 (SEC740N) (FRAGMENT).  
OS Staphylococcus aureus.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
OC Bacillus/Staphylococcus group; Staphylococcus.  
OX NCBI\_TaxID=1280.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=740N;  
RX MEDLINE=94011313; PubMed=8406814;  
RA Marr J.C., Lyon J.D., Roberson J.R., Lupher M., Bohach G.A.;  
RT "Characterization of novel type C staphylococcal enterotoxins:  
biological and evolutionary implications.";  
RL Infect. Immun. 61:4254-4262(1993).  
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION  
STAPHYLOCOCCAL FOOD POISONING SYNDROME.  
CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES  
PYROGENIC EXOTOXINS ARE ALL RELATED.  
EMBL: L13375; AAA26619.1; -.  
DR HSSP; P34071; 1SE2.  
DR InterPro; IPR001961; Staph\_Strep\_toxin.  
DR Pfam; PF01123; Staph\_Strep\_toxin; 1.  
DR PRINTS; PR00279; BACTRLTOXIN.  
DR PROSITE; PS00277; STAPH\_STREP\_TOXIN\_1; 1.  
DR PROSITE; PS00278; STAPH\_STREP\_TOXIN\_2; 1.  
KW Enterotoxin; Toxin; Superantigen.  
FT NON\_TER 1  
SQ SEQUENCE 239 AA; 27642 MW; C77009FA6BC8D645 CRC64;

Query Match 93.1%; Score 67; DB 2; Length 239;  
Best Local Similarity 83.3%; Pred. No. 0.00021;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 CMYGVTEHGN 12  
DB 110 CMYGVTEHGN 121

RESULT 7  
006533 PRELIMINARY; PRT; 239 AA.

AC 006533;  
DT 01-NOV-1996 (TREMblrel. 01, Created)  
DE 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
DE 01-JUN-2001 (TREMblrel. 17, Last annotation update)  
DE ENTEROTOXIN TYPE C (SECCOPELAND) (FRAGMENT).  
OS Staphylococcus aureus.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
OC Bacillus/Staphylococcus group; Staphylococcus.  
OX NCBI\_TaxID=1280.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MCORELAND;  
RX MEDLINE=94011313; PubMed=8406814;  
RA Marr J.C., Lyon J.D., Roberson J.R., Lupher M., Bohach G.A.;  
RT "Characterization of novel type C staphylococcal enterotoxins:  
biological and evolutionary implications.";

RL Infect. Immun. 61:4254-4262(1993).  
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION  
STAPHYLOCOCCAL FOOD POISONING SYNDROME.  
CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES  
PYROGENIC EXOTOXINS ARE ALL RELATED.  
EMBL: L13378; AAA26622.1; -.  
DR HSSP; P34071; 1STE.  
DR InterPro; IPR001961; Staph\_Strep\_toxin.  
DR Pfam; PF01123; Staph\_Strep\_toxin; 1.  
DR PRINTS; PR00279; BACTRLTOXIN.  
DR PROSITE; PS00277; STAPH\_STREP\_TOXIN\_1; 1.  
DR PROSITE; PS00278; STAPH\_STREP\_TOXIN\_2; 1.  
KW Enterotoxin; Toxin; Superantigen.  
FT NON\_TER 1  
SQ SEQUENCE 239 AA; 27651 MW; A21A954386AE8625 CRC64;

Query Match 93.1%; Score 67; DB 2; Length 239;  
Best Local Similarity 83.3%; Pred. No. 0.00021;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 CMYGVTEHGN 12  
DB 110 CMYGVTEHGN 121

RESULT 8  
006534 PRELIMINARY; PRT; 239 AA.

AC 006534;  
DT 01-NOV-1996 (TREMblrel. 01, Created)  
DE 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
DE 01-JUN-2001 (TREMblrel. 17, Last annotation update)  
DE ENTEROTOXIN TYPE C (SECOVINE) (FRAGMENT).  
OS Staphylococcus aureus.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
OC Bacillus/Staphylococcus group; Staphylococcus.  
OX NCBI\_TaxID=1280.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94011313; PubMed=8406814;  
RA Marr J.C., Lyon J.D., Roberson J.R., Lupher M., Bohach G.A.;  
RT "Characterization of novel type C staphylococcal enterotoxins:  
biological and evolutionary implications.";  
RL Infect. Immun. 61:4254-4262(1993).  
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION  
STAPHYLOCOCCAL FOOD POISONING SYNDROME.  
CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES  
PYROGENIC EXOTOXINS ARE ALL RELATED.  
EMBL: L13379; AAA26623.1; -.  
DR HSSP; P34071; 1SE2.  
DR InterPro; IPR001961; Staph\_Strep\_toxin.  
DR Pfam; PF01123; Staph\_Strep\_toxin; 1.  
DR PRINTS; PR00279; BACTRLTOXIN.  
DR PROSITE; PS00277; STAPH\_STREP\_TOXIN\_1; 1.  
DR PROSITE; PS00278; STAPH\_STREP\_TOXIN\_2; 1.  
KW Enterotoxin; Toxin; Superantigen.  
FT NON\_TER 1  
SQ SEQUENCE 239 AA; 27517 MW; F354742619C8D196 CRC64;

Query Match 93.1%; Score 67; DB 2; Length 239;  
Best Local Similarity 83.3%; Pred. No. 0.00021;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 CMYGVTEHGN 12  
DB 110 CMYGVTEHGN 121

RESULT 9  
006535 PRELIMINARY; PRT; 239 AA.

AC 006535;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)  
 DE ENTEROTOXIN TYPE C-3 (SEC3) (FRAGMENT).  
 OS Staphylococcus aureus.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
 OC Bacillus/Staphylococcus group; Staphylococcus.  
 OX NCBI\_TaxID=1280;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-FRI 909;  
 RA MEDLINE=94011313; PubMed=8406814;  
 RA Marr J.C., Lyon J.D., Roberson J.R., Luper M., Bohach G.A.;  
 RT "Characterization of novel type C Staphylococcal enterotoxins:  
 RT biological and evolutionary implications.";  
 RT Infect. Immun. 61:4254-4262(1993)  
 RL -1- DISASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION  
 CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.  
 CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES  
 CC PYROGENIC EXOTOXINS ARE ALL RELATED.  
 CC EMBL: L13377; AAA26621.1; -  
 DR HSP: P23313; IJCK.  
 DR InterPro: IPR001961; Staph\_Strep\_toxin.  
 DR Pfam: PF01123; Staph\_Strep\_toxin.1.  
 DR PRINTS: PR00279; BACTRITOXIN.  
 DR PROSITE: PS00277; STAPH\_STREP\_TOXIN\_1; 1.  
 DR PROSITE: PS00278; STAPH\_STREP\_TOXIN\_2; 1.  
 DR Enterotoxin; Toxin; Superantigen.  
 FT NON\_TER 1  
 SQ SEQUENCE 239 AA; 27648 MW; CC3CB3B04E119E0 CRC64;

Query Match 93.1%; Score 67; DB 2; Length 239;  
 Best Local Similarity 83.3%; Pred. No. 0.00021;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 CMYGVTEHGN 12  
 Db 110 CMYGVTEHGN 121

RESULT 10  
 O9F0L6 \ PRELIMINARY; PRT; 271 AA.  
 AC O9F0L6.  
 DT 01-MAR-2001 (TREMblrel. 16, Created)  
 DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)  
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)  
 DE STAPHYLOCOCCAL ENTEROTOXIN C-BOVINE.  
 GN SEC-BOV.  
 OS Staphylococcus aureus.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
 OC Bacillus/Staphylococcus group; Staphylococcus.  
 OX NCBI\_TaxID=1280;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=2056668; PubMed=11114901;  
 RA FitzGerald J.R., Monday S.R., Foster T.J., Bohach G.A., Hartigan P.J.,  
 RA Meaney W.J., Smyth C.J.;  
 RT "Characterization of a putative pathogenicity island from bovine  
 RT Staphylococcus aureus encoding multiple superantigens.";  
 RL J. Bacteriol. 183:63-70(2001).  
 EMBL: AF17235; AAG29599.1;  
 DR InterPro: IPR001961; Staph\_Strep\_toxin.  
 DR Pfam: PF01123; Staph\_Strep\_toxin.1.  
 DR PRINTS: PR00279; BACTRITOXIN.  
 SQ SEQUENCE 271 AA; 31267 MW; 3493F6228B042F10 CRC64;

Query Match 93.1%; Score 67; DB 2; Length 271;  
 Best Local Similarity 83.3%; Pred. No. 0.00024;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 CMYGVTEHGN 12  
 Db 142 CMYGVTEHGN 153

RESULT 11  
 Q9S5Z4 PRELIMINARY; PRT; 222 AA.  
 AC Q9S5Z4.  
 DT 01-MAY-2000 (TREMblrel. 13, Created)  
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)  
 DE EXOTOXIN TYPE A (FRAGMENT).  
 GN SP4.  
 OS Streptococcus pyogenes.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;  
 OC Streptococcus.  
 OX NCBI\_TaxID=1314;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=D633;  
 RA Bessen D.E., Izso M.W., Fiorentino T.R., Carling R.M., Beall B.;  
 RT "Genetic linkage of exotoxin alleles and emm gene markers for tissue  
 RT tropisms in group A streptococci.";  
 RT Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
 RL EMBL: AF029051; AAD21315.1; -  
 DR HSP: P08095; IB12.  
 DR InterPro: IPR001961; Staph\_Strep\_toxin.  
 DR Pfam: PF01123; Staph\_Strep\_toxin.1.  
 DR PRINTS: PR00279; BACTRITOXIN.  
 DR PROSITE: PS00277; STAPH\_STREP\_TOXIN\_1; 1.  
 DR PROSITE: PS00278; STAPH\_STREP\_TOXIN\_2; 1.  
 FT NON\_TER 1  
 FT NON\_TER 1  
 SQ SEQUENCE 222 AA; 25884 MW; 121F846092818F8 CRC64;

Query Match 87.5%; Score 63; DB 2; Length 222;  
 Best Local Similarity 83.3%; Pred. No. 0.001;  
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 OY 1 CMYGVTEHGN 12  
 Db 108 CMYGVTEHGN 119

RESULT 12  
 Q9R931 PRELIMINARY; PRT; 222 AA.  
 AC Q9R931.  
 DT 01-MAY-2000 (TREMblrel. 13, Created)  
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)  
 DE EXOTOXIN A (FRAGMENT).  
 GN SP4.  
 OS Streptococcus pyogenes.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;  
 OC Streptococcus.  
 OX NCBI\_TaxID=1314;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=D709;  
 RA Bessen D.E., Izso M.W., Fiorentino T.R., Carling R.M.,  
 RA Hollingshead S.K., Beall B.;  
 RT "Genetic linkage of exotoxin alleles and emm gene markers for tissue  
 RT tropism in group A streptococci.";  
 RT Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.  
 RL EMBL: AF055698; AAD11624.1; -  
 DR HSP: P08095; IB12.  
 DR InterPro: IPR001961; Staph\_Strep\_toxin.  
 DR Pfam: PF01123; Staph\_Strep\_toxin.1.  
 DR PRINTS: PR00279; BACTRITOXIN.

```
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
FT NON_TER 222
SO SEQUENCE 222 AA; 25759 MW; 48BB7ADDCD91FBA3 CRC64;

Query Match
Best Local Similarity 87.5%; Score 63; DB 2; Length 222;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGVTEHEGN 12
   1:||||| ||||
Db 108 CIYGVTHNEGN 119

RESULT 13
O54696 PRELIMINARY; PRT; 236 AA.
AC O54696;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE TYPE A EXOTOXIN PRECURSOR (FRAGMENT).
GN SPEA.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Streptococcus.
NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS156;
MEDLINE=92044323; PubMed=1940804;
RA Nelson K., Schlievert P.M., Selander R.K., Musser J.M.;
RT "Characterization and clonal distribution of four alleles of the speA
   gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
   Streptococcus pyogenes.";
   J. Exp. Med. 174:1271-1274(1991).
EMBL; X61573; CAA43771.1; -.
DR HSSP; P08095; 1B1Z.
DR InterPro; IPR001961; Staph_Strep_toxin.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Signal.
FT NON_TER 1
FT SIGNAL <1 22 POTENTIAL.
FT CHAIN 23 >236 TYPE A EXOTOXIN.
FT NON_TER 236
FT NON_TER 236
SO SEQUENCE 236 AA; 27575 MW; 70F54120E79127DF CRC64;

Query Match
Best Local Similarity 87.5%; Score 63; DB 2; Length 236;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGVTEHEGN 12
   1:||||| ||||
Db 120 CIYGVTHNEGN 131

RESULT 14
O54779 PRELIMINARY; PRT; 236 AA.
AC O54779; O54613; O54736; O54740; O54741;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE TYPE A EXOTOXIN PRECURSOR (FRAGMENT).
GN SPEA.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
```

```
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS624 AND MGAS158 AND MGAS485 AND MGAS491, AND MGAS495;
RC MEDLINE=92044323; PubMed=1940804;
RA Nelson K., Schlievert P.M., Selander R.K., Musser J.M.;
RT "Characterization and clonal distribution of four alleles of the speA
   gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
   Streptococcus pyogenes.";
   J. Exp. Med. 174:1271-1274(1991).
EMBL; X61569; CAA43767.1; -.
DR EMBL; X61572; CAA43770.1; -.
DR EMBL; X61568; CAA43766.1; -.
DR EMBL; X61570; CAA43768.1; -.
DR EMBL; X61571; CAA43769.1; -.
DR HSSP; P08095; 1B1Z.
DR InterPro; IPR001961; Staph_Strep_toxin.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Signal.
FT NON_TER 1
FT SIGNAL <1 22 POTENTIAL.
FT CHAIN 23 >236 TYPE A EXOTOXIN.
FT NON_TER 236
FT NON_TER 236
SO SEQUENCE 236 AA; 27468 MW; 29DF2AD575623A84 CRC64;

Query Match
Best Local Similarity 87.5%; Score 63; DB 2; Length 236;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGVTEHEGN 12
   1:||||| ||||
Db 120 CIYGVTHNEGN 131

RESULT 15
O57453 PRELIMINARY; PRT; 236 AA.
AC O57453;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE TYPE A EXOTOXIN PRECURSOR (FRAGMENT).
GN SPEA.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Streptococcus.
NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS496;
MEDLINE=92044323; PubMed=1940804;
RA Nelson K., Schlievert P.M., Selander R.K., Musser J.M.;
RT "Characterization and clonal distribution of four alleles of the speA
   gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
   Streptococcus pyogenes.";
   J. Exp. Med. 174:1271-1274(1991).
EMBL; X61562; CAA43760.1; -.
DR EMBL; X61563; CAA43761.1; -.
DR EMBL; X61567; CAA43765.1; -.
DR EMBL; X61561; CAA43759.1; -.
DR EMBL; X61564; CAA43762.1; -.
DR EMBL; X61565; CAA43763.1; -.
DR EMBL; X61566; CAA43764.1; -.
DR HSSP; P08095; 1B1Z.
DR InterPro; IPR001961; Staph_Strep_toxin.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
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DR PROSITE: PS00278; STAPH\_STREP\_TOXIN\_2; 1.  
 KW Signal.  
 FT NON\_TER 1 1  
 FT SIGNAL <1 22 POTENTIAL.  
 FT CHAIN 23 >236 TYPE A EXOTOXIN.  
 FT NON\_TER 236 236  
 SQ SEQUENCE 236 AA: 27484 MW: 2EF7F41AAC853600 CRC64;

Query Match 87.5%; Score 63; DB 2; Length 236;  
 Best Local Similarity 83.3%; Pred. No. 0.0011;  
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGGVTEHEGN 12  
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 Db 120 CIYGGVTNHEGN 131

Search completed: January 2, 2002, 20:52:02  
 Job time: 227 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 2, 2002, 20:48:13 ; Search time 77.31 Seconds  
(without alignments)  
11.498 Million cell updates/sec

Title: US-09-335-581A-34  
Perfect score: 71  
Sequence: 1 CMWGVTLHEGN 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues  
Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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22: /SIDS2/gcgdata/geneseq/geneseqp/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	64	90.1	12	19	AAW72422
2	64	90.1	12	21	AAV97836
3	64	90.1	12	21	AAV97846
4	64	90.1	12	22	AAV72176
5	64	90.1	12	22	AAV72184
6	64	90.1	14	19	AAW72424
7	64	90.1	14	21	AAV97840
8	64	90.1	14	22	AAV72178
9	64	90.1	36	19	AAW72426
10	64	90.1	36	21	AAV97842
11	64	90.1	36	22	AAV72180

12	64	90.1	38	19	AAW72427	Peptide #6 for red
13	64	90.1	38	21	AAV97843	Staphylococcal/str
14	64	90.1	38	22	AAV72181	Peptide #6348, der
15	64	90.1	238	12	AAK13208	Staphylococcal ent
16	64	90.1	238	14	AAK45016	Staphylococcal ent
17	64	90.1	238	22	AAK67343	Staphylococcal ent
18	64	90.1	239	12	AAK13207	Staphylococcal ent
19	64	90.1	239	14	AAK45015	Staphylococcal ent
20	64	90.1	239	20	AAV06254	Staphylococcal gro
21	64	90.1	239	20	AAV06255	Staphylococcal gro
22	64	90.1	239	20	AAV06256	Staphylococcal gro
23	64	90.1	239	20	AAV06257	Staphylococcal gro
24	64	90.1	239	20	AAV06258	Staphylococcal gro
25	64	90.1	239	20	AAV06251	Staphylococcal gro
26	64	90.1	239	20	AAV06252	Staphylococcal gro
27	64	90.1	239	20	AAV06253	Staphylococcal gro
28	64	90.1	239	22	AAK67342	Staphylococcal ent
29	64	90.1	266	21	AAV70108	Staphylococcal ent
30	62	87.3	12	21	AAV97844	Staphylococcal ent
31	62	87.3	12	21	AAV97848	Staphylococcal ent
32	62	87.3	12	22	AAV72182	Peptide from regio
33	62	87.3	12	22	AAV72186	Peptide from regio
34	62	87.3	23	17	AAW04492	Staphylococcal ent
35	62	87.3	23	20	AAW73919	Staphylococcal ent
36	62	87.3	230	12	AAK13204	Staphylococcal ent
37	62	87.3	230	14	AAK45012	Staphylococcal ent
38	62	87.3	230	22	AAK67339	Staphylococcal ent
39	62	87.3	233	12	AAK13203	Staphylococcal ent
40	62	87.3	233	18	AAK45011	Staphylococcal ent
41	62	87.3	233	18	AAW35373	Staphylococcal ent
42	62	87.3	233	18	AAW06738	Staphylococcal ent
43	62	87.3	233	21	AAV70103	Mutant Staphylococ
44	62	87.3	233	21	AAV54463	Amino acid sequenc
45	62	87.3	233	22	AAK67338	Staphylococcal ent

## ALIGNMENTS

RESULT 1  
ID AAW72422 standard; peptide: 12 AA.  
XX  
AC AAW72422;  
XX  
DT 22-DEC-1998 (first entry)  
XX  
DE Peptide #1 for reducing symptoms of toxic shock syndrome.  
XX  
KW Toxic shock syndrome; immunogenic response; bacterial infection;  
KW staphylococcal enterotoxin; streptococcal pyrogenic toxin; antibody;  
KW autoimmune disease.  
XX  
OS Synthetic.  
OS Staphylococcus sp.  
OS Streptococcus sp.  
XX  
PN W09845325-A1.  
XX  
PD 15-OCT-1998.  
XX  
PF 01-APR-1998; 98WO-US06663.  
XX  
PR 07-APR-1997; 97US-0838413.  
XX  
PA (UYRQ ) UNTV ROCKEFELLER.  
XX  
PI Bannan JD, Zabriskie JB;  
XX WPI: 1998-568335/48.  
XX  
DR New peptides that generate antibodies against staphylococcal and  
XX streptococcal toxins - used to diagnose, treat or prevent toxic  
PT

PT shock and autoimmune diseases  
XX  
XX Claim 4; Page 53; 69pp; English.  
XX  
CC The present invention describes peptides having consensus sequences #1  
CC or #2, optionally as part of a larger molecule of size at least 6-8 kD.  
CC Where consensus sequence #1 and #2 are: X25X26YGX17X23X4X3N #1,  
CC K66X78X910X11X12X13DX14X15X16RX17X18X20X21X22X23X24Y #2, where  
CC X1, X8, X13 and X24 = L, I or V; X3, X25 and X26 = any amino acid (aa)  
CC or are absent; X27 = L or Y; all other X may be any aa. The peptides  
CC can be used to generate serum antibodies (Ab) that bind at least one  
CC staphylococcal enterotoxin (SE) or streptococcal endotoxin (SE). Ab  
CC are used: (i) for diagnostic detection of SPEA or SEA, SEB and SED. In  
CC usual immunoassays; (ii) to inhibit blastogenesis of human mononuclear  
CC cells in presence of these toxins (i.e. to protect against or alleviate  
CC toxic shock or autoimmune disease associated with bacterial infections);  
CC and (iii) for passive immunisation against effects of the toxins. The  
CC peptides generate Ab that are cross-reactive with toxins from a variety  
CC of bacteria. The present sequence represents a specifically claimed  
CC example of a peptide of the present invention.  
XX  
SQ Sequence 12 AA:  
Query Match 90.1%; Score 64; DB 19; Length 12;  
Best Local Similarity 91.7%; Pred. No. 7.1e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Db 1 CMYGVTLHEGN 12  
1 cmygvtehegn 12  
RESULT 2  
AAV97838  
ID AAV97838 standard; peptide: 12 AA.  
XX  
AC AAV97838;  
XX  
XX 29-AUG-2000 (first entry)  
DE Staphylococcal/streptococcal pyrogenic toxin-derived peptide, 6343.  
XX  
XX Pyrogenic exotoxin; enterotoxin; streptococcal infection;  
KM staphylococcal infection; septic shock; toxic shock; vaccine;  
KM antibody.  
XX  
OS Synthetic.  
OS Staphylococcus aureus.  
OS Streptococcus sp. Group A'.  
XX  
XX MO200020598-A1.  
XX  
XX 13-APR-2000.  
PD  
XX  
XX 24-SEP-1999; 99WO-US22180.  
PF  
XX  
XX 07-OCT-1998; 98US-0168303.  
PR  
XX 18-JUN-1999; 99US-0335581.  
PR  
XX  
XX (UYRQ ) UNIV ROCKEFELLER.  
PA  
XX  
XX Bannan JD, Visvanathan K, Zabriskie JB;  
PI WPI; 2000-303782/26.  
XX  
XX  
XX Peptides useful for preventing and reducing the symptoms of toxic shock  
PT syndrome and septic shock from staphylococcal and streptococcal  
PT infections -  
XX  
XX Claim 4; Page 88; 115pp; English.  
PS  
XX The invention relates to novel peptides (AAV97838-Y97843) comprising a

CC consensus amino acid sequence derived from two conserved regions  
CC (regions 1 and 2) of Staphylococcus aureus enterotoxins and  
CC streptococcal pyrogenic toxins. Consensus region 1a (a preferred  
CC consensus region 1) has the sequence X25-X26-Y-G-X1-T-X2-X3-X4-X5-N  
CC (AAV97863) and consensus region 2a (a preferred consensus region 2) has  
CC the sequence K-X6-X7-X8-  
CC X9-X10-X11-X12-X13-D-X14-X15-X16-R-X17-X18-X27-X19-X20-X21-X22-X23-X24-Y  
CC (AAV97864), where: X1, X8, X13 and X24 are each independently selected  
CC from L, I and V; X2, X4, X5, X6, X7, X9, X10, X11, X12, X14, X15, X16,  
CC X17, X18, X19, X20, X21, X22 and X23 are each independently selected from  
CC the group consisting of any amino acid;  
CC X3, X5 and X26 are each independently selected from the group consisting  
CC of any amino acid and of no amino acid;  
CC X27 is either L or Y.  
CC The invention also relates to serum antibodies induced by the peptides  
CC which provide protection against, or reduce the severity of toxic shock  
CC and septic shock caused by the staphylococcal and streptococcal  
CC pyrogenic toxins. The pyrogenic exotoxins of Group A streptococci and  
CC the enterotoxins of Staphylococcus aureus (which are also pyrogenic  
CC exotoxins) constitute a family of structurally related toxins which  
CC share similar biological activities. They stimulate CD4+, CD8+ and  
CC gamma-delta+ T-cells by binding the beta-chain variable region (V-beta)  
CC elements on the lateral face of the T-cell receptor (TCR) while  
CC simultaneously binding the lateral face of the class II major  
CC histocompatibility complex (MHC) of antigen presenting cells. This causes  
CC aberrant proliferation of T-cells, which stimulates other components of  
CC the immune system, causing injury to the host. The peptides are used to  
CC prevent, treat or protect against toxic shock and septic shock resulting  
CC from bacterial infections in mammals, particularly humans. The peptides  
CC are used for inducing serum antibodies that bind at least one  
CC staphylococcal enterotoxin or streptococcal exotoxin and both the  
CC peptides and antibodies can be used in diagnostic assays to aid in the  
CC diagnosis of disease related to the presence of bacterial toxins. Nucleic  
CC acids encoding a peptide of the invention can be used for the production  
CC of the peptides for diagnostic reagents, as vaccines and for therapies  
CC for pyrogenic exotoxin related diseases. Vectors expressing high levels  
CC of the peptides can be used in immunotherapy and immunoprophylaxis when  
CC expressed in humans. The antibodies are used for passive immunisation or  
CC therapy to prevent or increase resistance to toxic shock syndrome or  
CC septic shock and to ameliorate the effects of conditions associated with  
CC the presence of staphylococcal or streptococcal pyrogenic toxins. The  
CC amino acid sequences of the peptides are sufficiently common that they  
CC can be used for eliciting antibodies which are cross-reactive with toxins  
CC derived from various bacteria. Sequences AAV97838-Y978343 represent the  
CC synthetic peptides based on consensus consensus regions 1 and 2 of  
CC Staphylococcus aureus and Group A streptococcal pyrogenic toxins.  
CC These peptides can be administered to a mammal to raise serum antibodies  
CC for protection against or amelioration of toxic or septic shock.  
XX  
XX  
SQ Sequence 12 AA:  
Query Match 90.1%; Score 64; DB 21; Length 12;  
Best Local Similarity 91.7%; Pred. No. 7.1e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Db 1 CMYGVTLHEGN 12  
1 cmygvtehegn 12  
RESULT 3  
AAV97846  
ID AAV97846 standard; peptide: 12 AA.  
XX  
XX  
XX AAV97846;  
XX  
XX 29-AUG-2000 (first entry)  
DE Staphylococcus aureus enterotoxin SEC, conserved region 1.  
XX  
XX Staphylococcal infection; enterotoxin; septic shock; toxic shock;  
KM vaccine; antibody.  
KM



XX OS Staphylococcus aureus.  
 XX PM WO200020598-A1.  
 XX PD 13-APR-2000.  
 XX PF 24-SEP-1999; 99WO-US22180.  
 XX PR 07-OCT-1998; 98US-0168303.  
 XX PR 18-JUN-1999; 99US-0335381.  
 XX PA (UYRO ) UNIV ROCKEFELLER.  
 XX PI Bannan JD, Visvanathan K, Zabriskie JB:  
 XX WPI: 2000-303782/26.  
 XX DR  
 XX PT Peptides useful for preventing and reducing the symptoms of toxic shock  
 XX PT syndrome and septic shock from staphylococcal and streptococcal  
 XX PT infections -  
 XX PS Example 1; Page 72; 115pp; English.  
 XX CC The invention relates to novel peptides (AA97838-Y97843) comprising a  
 XX CC consensus amino acid sequence derived from two conserved regions  
 XX CC (regions 1 and 2) of Staphylococcus aureus enterotoxins and  
 XX CC streptococcal pyrogenic toxins. Consensus region 1a (a preferred  
 XX CC consensus region 1) has the sequence X25-X26-Y-G-G-X1-T-X2-X3-X4-X5-N  
 XX CC (AA97863) and consensus region 2a (a preferred consensus region 2) has  
 XX CC the sequence K-X6-X7-X8-  
 XX CC X9-X10-X11-X12-X13-D-X14-X15-X16-R-X17-X18-X27-X19-X20-X21-X22-X23-X24-Y  
 XX CC (AA97864), where: X1, X8, X13 and X24 are each independently selected  
 XX CC from L, I and V; X2, X4, X5, X6, X7, X9, X10, X11, X12, X14, X15, X16,  
 XX CC X17, X18, X19, X20, X21, X22 and X23 are each independently selected from  
 XX CC the group consisting of any amino acid;  
 XX CC X3, X5 and X26 are each independently selected from the group consisting  
 XX CC of any amino acid and of no amino acid;  
 XX CC X27 is either L or Y.  
 XX CC The invention also relates to serum antibodies induced by the peptides  
 XX CC which provide protection against, or reduce the severity of toxic shock  
 XX CC and septic shock caused by the staphylococcal and streptococcal  
 XX CC pyrogenic toxins. The pyrogenic exotoxins of Group A streptococci and  
 XX CC the enterotoxins of Staphylococcus aureus (which are also pyrogenic  
 XX CC exotoxins) constitute a family of structurally related toxins which  
 XX CC share similar biological activities. They stimulate CD4+ and  
 XX CC gamma-delta+ T-cells by binding the beta-chain variable region (V-beta)  
 XX CC elements on the lateral face of the T-cell receptor (TCR) while  
 XX CC simultaneously binding the lateral face of the class II major  
 XX CC histocompatibility complex (MHC) of antigen presenting cells. This causes  
 XX CC aberrant proliferation of T-cells, which stimulates other components of  
 XX CC the immune system, causing injury to the host. The peptides are used to  
 XX CC prevent, treat or protect against toxic shock and septic shock resulting  
 XX CC from bacterial infections in mammals, particularly humans. The peptides  
 XX CC are used for inducing serum antibodies that bind at least one  
 XX CC staphylococcal enterotoxin or streptococcal exotoxin and both the  
 XX CC peptides and antibodies can be used in diagnostic assays to aid in the  
 XX CC diagnosis of disease related to the presence of bacterial toxins. Nucleic  
 XX CC acids encoding a peptide of the invention can be used for the production  
 XX CC of the peptides for diagnostic reagents, as vaccines and for therapies  
 XX CC for pyrogenic exotoxin related diseases. Vectors expressing high levels  
 XX CC of the peptides can be used in immunotherapy and immunoprophylaxis when  
 XX CC expressed in humans. The antibodies are used for passive immunisation or  
 XX CC therapy to prevent or increase resistance to toxic shock syndrome or  
 XX CC septic shock and to ameliorate the effects of conditions associated with  
 XX CC the presence of staphylococcal or streptococcal pyrogenic toxins. The  
 XX CC amino acid sequences of the peptides are sufficiently common that they  
 XX CC can be used for eliciting antibodies which are cross-reactive with toxins  
 XX CC derived from various bacteria. Sequences AA97844-Y97852 represent  
 XX CC conserved region 1 of various Staphylococcus aureus enterotoxins and  
 XX CC Group A streptococcal pyrogenic exotoxins.  
 XX CC Sequence 12 AA:

Query Match 90.1%; Score 64; DB 21; Length 12;  
 Best Local Similarity 83.3%; Pred. No. 7,1e-05;  
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 Db. 1 CMYGGVTLHEGN 12  
 1 CMYGGVTLKHEGN 12

## RESULT 4

AA972176  
 ID AA972176 standard; peptide; 12 AA.

AC AA972176;  
 XX

DT 24-APR-2001 (first entry)  
 XX

DE Peptide #6343, derived from streptococcal and staphylococcal toxins.  
 XX

KW Mononuclear cell; blastogenesis; inhibitor; HIV; replication; therapy;  
 KW staphylococcal enterotoxin; human immunodeficiency virus; T cell;  
 KW streptococcal pyrogenic exotoxin; autoimmune disease; immunisation.  
 XX

OS Streptococcus sp.  
 XX

OS Staphylococcus sp.  
 XX

PM WO200078790-A2.  
 XX

PD 28-DEC-2000.  
 XX

PF 16-JUN-2000; 2000WO-US16680.  
 XX

PR 18-JUN-1999; 99US-0336627.  
 XX

PA (UYRO ) UNIV ROCKEFELLER.  
 XX

PI Visvanathan K, Zabriskie JB;  
 XX

DR WPI: 2001-080820/09.  
 XX

PT Providing protection against, and reducing the severity of, human  
 PT immunodeficiency virus infections and associated deleterious effects,  
 PT using peptides from homologous sequences of staphylococcal and  
 PT streptococcal toxins -  
 XX

PS Claim 5; Page 38; 76pp; English.  
 XX

CC The present sequence is peptide #6343, derived from region 1 of  
 CC the homologous sequences of staphylococcal enterotoxin and  
 CC streptococcal pyrogenic exotoxin.  
 CC The peptide, nucleic acid encoding the peptide and antibody (Ab) produced  
 CC against the peptide are useful for inhibiting blastogenesis of  
 CC mononuclear cells (eg. T cells) in the presence of human immunodeficiency  
 CC virus (HIV), inhibiting HIV replication and protecting a mammal against  
 CC the deleterious effects of HIV. The peptide is also used to ameliorate  
 CC the effects of autoimmune diseases associated with the presence of HIV.  
 CC The Ab is used for passively immunising a mammal against the deleterious  
 CC effects of HIV.  
 XX

PS Sequence 12 AA;  
 XX

SQ Sequence 12 AA;  
 XX

Query Match 90.1%; Score 64; DB 22; Length 12;  
 Best Local Similarity 91.7%; Pred. No. 7,1e-05;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGGVTLHEGN 12  
 |||||  
 Db 1 CMYGGVTLKHEGN 12

```

RESULT 5
AAV72184
ID AAV72184 standard; peptide: 12 AA.
XX
AC AAV72184;
XX
DT 24-APR-2001 (first entry)
XX
DE Peptide from region 1 of staphylococcal enterotoxin SEC.
XX
KM Mononuclear cell; blastogenesis; inhibitor; HIV; replication; therapy;
KM staphylococcal enterotoxin; human immunodeficiency virus; T cell;
KM autoimmune disease; immunisation.
XX
OS Staphylococcus sp.
XX
PN MO200078790-A2.
XX
PD 28-DEC-2000.
XX
PF 16-JUN-2000; 2000WO-US16680.
XX
PR 18-JUN-1999; 99US-0336627.
XX
PA (UVRQ ) UNIV ROCKEFELLER.
XX
PI Visvanathan K, Zabriskie JB;
XX
DR WPI; 2001-080820/09.
XX
PT Providing protection against, and reducing the severity of, human
PT immunodeficiency virus infections and associated deleterious effects,
PT using peptides from homologous sequences of staphylococcal and
PT streptococcal toxins
XX
PS Disclosure; Page 36; 76pp; English.
XX
XX The present sequence is a peptide from region 1 of staphylococcal
XX enterotoxin SEC.
XX The peptide, nucleic acid encoding the peptide and antibody (Ab) produced
XX against the peptide are useful for inhibiting blastogenesis of
XX mononuclear cells (eg. T cells) in the presence of human immunodeficiency
XX virus (HIV), inhibiting HIV replication and protecting a mammal against
XX the deleterious effects of HIV. The peptide is also used to ameliorate
XX the effects of autoimmune diseases associated with the presence of HIV.
XX The Ab is used for passively immunising a mammal against the deleterious
XX effects of HIV.
XX
SQ Sequence 12 AA;

```

Query Match 90.1%; Score 64; DB 22; Length 12;  
 Best Local Similarity 83.3%; Pred. No. 7.1e-05;  
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 CMYGGVTLHEGN 12
DB 1 cmysgltkhegn 12

```

RESULT 6  
 AAV72424  
 ID AAV72424 standard; peptide: 14 AA.  
 XX  
 AC AAV72424;  
 XX  
 DT 22-DEC-1998 (first entry)  
 XX  
 DE Peptide #3 for reducing symptoms of toxic shock syndrome.  
 XX  
 KM Toxic shock syndrome; immunogenic response; bacterial infection;  
 KM staphylococcal enterotoxin; streptococcal pyrogenic toxin; antibody;  
 KM autoimmune disease.

```

XX
OS Synthetic.
OS Staphylococcus sp.
OS Streptococcus sp.
XX
PN MO9845325-A1.
XX
PD 15-OCT-1998.
XX
PF 01-APR-1998; 98WO-US06663.
XX
PR 07-APR-1997; 97US-0838413.
XX
PA (UVRQ ) UNIV ROCKEFELLER.
XX
PI Bannan JD, Zabriskie JB;
XX
DR WPI; 1998-568335/48.
XX
PD New peptides that generate antibodies against staphylococcal and
PT streptococcal toxins - used to diagnose, treat or prevent toxic
PT shock and autoimmune diseases
XX
PS Claim 4; Page 53; 69pp; English.
XX
XX The present invention describes peptides having consensus sequences #1
XX or #2, optionally as part of a larger molecule of size at least 6-8 kD.
XX Where consensus sequence #1 and #2 are: X25X26YGGX17X23X4X5N #1,
XX KX6X78X9X10X11X12X13DX14X15X16RX17X18X27X19X20X21X22X23X24Y #2, where
XX X1, X8, X13 and X24 = L, I or V; X3, X25 and X26 = any amino acid (aa)
XX or are absent; X27 = L or Y; all other X may be any aa. The peptides
XX can be used to generate serum antibodies (Ab) that bind at least one
XX staphylococcal enterotoxin (SE) or streptococcal endotoxin (SE). Ab
XX are used: (i) for diagnostic detection of SPEA or SEA, SEB and SED, in
XX usual immunoassays; (ii) to inhibit blastogenesis of human mononuclear
XX cells in presence of these toxins (i.e. to protect against or alleviate
XX toxic shock or autoimmune disease associated with bacterial infections);
XX and (iii) for passive immunisation against effects of the toxins. The
XX peptides generate Ab that are cross-reactive with toxins from a variety
XX of bacteria. The present sequence represents a specifically claimed
XX example of a peptide of the present invention.
XX
SQ Sequence 14 AA;

```

Query Match 90.1%; Score 64; DB 19; Length 14;  
 Best Local Similarity 91.7%; Pred. No. 8.4e-05;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 CMYGGVTLHEGN 12
DB 1 cmysgvtkehegn 12

```

RESULT 7  
 AAV97840  
 ID AAV97840 standard; peptide: 14 AA.  
 XX  
 AC AAV97840;  
 XX  
 DT 29-AUG-2000 (first entry)  
 XX  
 DE Staphylococcal/streptococcal pyrogenic toxin-derived peptide, 6344.  
 XX  
 KM Pyrogenic exotoxin; enterotoxin; streptococcal infection;  
 KM staphylococcal infection; septic shock; toxic shock; vaccine;  
 KM antibody.  
 XX  
 OS Synthetic.  
 OS Staphylococcus aureus.  
 OS Streptococcus sp. 'Group A'.  
 XX  
 PN MO200020598-A1.

XX 13-APR-2000.  
 PD  
 PF 24-SEP-1999; 99MO-US22180.  
 XX  
 PR 07-OCT-1998; 9805-0168303.  
 PR 18-JUN-1999; 99US-0335581.  
 XX  
 PA (UYRQ ) UNIV ROCKEFELLER.  
 PI Bannan JD, Visvanathan K, Zabriskie JB;  
 DR WPI: 2000-303782/26.  
 XX  
 PT Peptides useful for preventing and reducing the symptoms of toxic shock  
 PT syndrome and septic shock from staphylococcal and streptococcal  
 PT infections -  
 XX  
 PS Claim 4; Page 88; 115pp; English.  
 XX  
 CC The invention relates to novel peptides (AAV97838-Y97843) comprising a  
 CC consensus amino acid sequence derived from two conserved regions  
 CC (regions 1 and 2) of Staphylococcus aureus enterotoxins and  
 CC streptococcal pyrogenic toxins. Consensus region 1a (a preferred  
 CC consensus region 1) has the sequence X25-X26-Y-G-G-X1-T-X2-X3-X4-X5-N  
 CC (AAV97863) and consensus region 2a (a preferred consensus region 2) has  
 CC the sequence K-X6-X7-X8-  
 CC X3-X10-X11-X12-X13-D-X14-X15-X16-R-X17-X18-X27-X19-X20-X21-X22-X23-X24-Y  
 CC (AAV97864), where: X1, X8, X13 and X24 are each independently selected  
 CC from L, I and V; X2, X4, X5, X6, X7, X9, X10, X11, X12, X14, X15, X16,  
 CC X17, X18, X19, X20, X21, X22 and X23 are each independently selected from  
 CC the group consisting of any amino acid;  
 CC X3, X5 and X26 are each independently selected from the group consisting  
 CC of any amino acid and of no amino acid;  
 CC X27 is either L or Y.  
 CC The invention also relates to serum antibodies induced by the peptides  
 CC which provide protection against, or reduce the severity of toxic shock  
 CC and septic shock caused by the staphylococcal and streptococcal  
 CC pyrogenic toxins. The pyrogenic exotoxins of Group A streptococci and  
 CC the enterotoxins of Staphylococcus aureus (which are also pyrogenic  
 CC exotoxins) constitute a family of structurally related toxins which  
 CC share similar biological activities. They stimulate CD4<sup>+</sup>, CD8<sup>+</sup> and  
 CC gamma-delta-T-cells by binding the beta-chain variable region (V-beta)  
 CC elements on the lateral face of the T-cell receptor (TCR) while  
 CC simultaneously binding the lateral face of the class II major  
 CC histocompatibility complex (MHC) of antigen presenting cells. This causes  
 CC aberrant proliferation of T-cells, which stimulates other components of  
 CC the immune system, causing injury to the host. The peptides are used to  
 CC prevent, treat or protect against toxic shock and septic shock resulting  
 CC from bacterial infections in mammals, particularly humans. The peptides  
 CC are used for inducing serum antibodies that bind at least one  
 CC staphylococcal enterotoxin or streptococcal exotoxin and both the  
 CC peptides and antibodies can be used in diagnostic assays to aid in the  
 CC diagnosis of disease related to the presence of bacterial toxins. Nucleic  
 CC acids encoding a peptide related to the invention can be used for the production  
 CC of the peptides for diagnostic reagents, as vaccines and for therapies  
 CC for pyrogenic exotoxin related diseases. Vectors expressing high levels  
 CC of the peptides can be used in immunotherapy and immunoprophylaxis when  
 CC expressed in humans. The antibodies are used for passive immunisation  
 CC therapy to prevent or increase resistance to toxic shock syndrome or  
 CC septic shock and to ameliorate the effects of conditions associated with  
 CC the presence of staphylococcal or streptococcal pyrogenic toxins. The  
 CC amino acid sequences of the peptides are sufficiently common that they  
 CC can be used for eliciting antibodies which are cross-reactive with toxins  
 CC derived from various bacteria. Sequences AAV97838-Y97833 represent the  
 CC synthetic peptides based on consensus consensus regions 1 and 2 of  
 CC Staphylococcus aureus and Group A streptococcal pyrogenic toxins.  
 CC These peptides can be administered to a mammal to raise serum antibodies  
 CC for protection against or amelioration of toxic or septic shock.  
 CC  
 CC Sequence 14 AA:  
 CC  
 CC SQ

Query Match 90.1%; Score 64; DB 21; Length 14;  
 Best Local Similarity 91.7%; Pred. No. 8.4e-05;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGVTLHEGN 12  
 |||||  
 Db 1 cmgyvtehegn 12

## RESULT 8

AAV72178  
 ID AAV72178 standard; peptide; 14 AA.  
 XX  
 AC AAV72178;  
 XX  
 DT 24-APR-2001 (first entry)  
 XX  
 DE Peptide #6344, derived from streptococcal and staphylococcal toxins.  
 XX  
 KW Mononuclear cell; blastogenesis; inhibitor; HIV; replication; therapy;  
 KW staphylococcal enterotoxin; human immunodeficiency virus; T cell;  
 KW streptococcal pyrogenic exotoxin; autoimmune disease; immunisation.  
 XX  
 OS Streptococcus sp.  
 XX Staphylococcus sp.  
 PN W0200078790-A2.  
 XX  
 PD 28-DEC-2000.  
 XX  
 PF 16-JUN-2000; 2000WO-US16680.  
 XX  
 PR 18-JUN-1999; 99US-0336627.  
 XX  
 PA (UYRQ ) UNIV ROCKEFELLER.  
 PI Visvanathan K, Zabriskie JB;  
 DR WPI: 2001-080820/09.  
 XX  
 PT Providing protection against, and reducing the severity of, human  
 PT immunodeficiency virus infections and associated deleterious effects,  
 PT using peptides from homologous sequences of staphylococcal and  
 PT streptococcal toxins -  
 XX  
 XX  
 PS Claim 5; Page 38; 76pp; English.  
 XX  
 CC The present sequence is peptide #6344, a cross-linked polymer derived  
 CC from the homologous sequences of staphylococcal enterotoxin and  
 CC streptococcal pyrogenic exotoxin.  
 CC The peptide, nucleic acid encoding the peptide and antibody (Ab) produced  
 CC against the peptide are useful for inhibiting blastogenesis of  
 CC mononuclear cells (eg. T cells) in the presence of human immunodeficiency  
 CC virus (HIV), inhibiting HIV replication and protecting a mammal against  
 CC the deleterious effects of HIV. The peptide is also used to ameliorate  
 CC the effects of autoimmune diseases associated with the presence of HIV.  
 CC The Ab is used for passively immunising a mammal against the deleterious  
 CC effects of HIV.  
 CC  
 CC Sequence 14 AA:  
 CC  
 CC SQ

Query Match 90.1%; Score 64; DB 22; Length 14;  
 Best Local Similarity 91.7%; Pred. No. 8.4e-05;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGVTLHEGN 12  
 |||||  
 Db 1 cmgyvtehegn 12

RESULT 9  
 AAV72426

ID AAW72426 standard; peptide; 36 AA.  
XX  
AC AAW72426;  
XX  
DT 22-DEC-1998 (first entry)  
XX  
DE Peptide #5 for reducing symptoms of toxic shock syndrome.  
XX  
KW Toxic shock syndrome; immunogenic response; bacterial infection;  
KW staphylococcal enterotoxin; streptococcal pyrogenic toxin; antibody;  
KW autoimmune disease.  
XX  
OS Synthetic.  
OS Staphylococcus sp.  
OS Streptococcus sp.  
XX  
PN W09845325-A1.  
XX  
PD 15-OCT-1998.  
XX  
PF 01-APR-1998; 98WO-US06663.  
XX  
PR 07-APR-1997; 97US-0838413.  
XX  
PA (UYRQ ) UNIV ROCKEFELLER.  
XX  
PI Bannan JD, Zabriskie JB;  
XX  
PI MPI; 1998-56835/48.  
XX  
PT New peptides that generate antibodies against staphylococcal and  
PT streptococcal toxins - used to diagnose, treat or prevent toxic  
PT shock and autoimmune diseases  
XX  
PS Claim 4; Page 54; 69pp; English.  
XX  
CC The present invention describes peptides having consensus sequences #1  
CC or #2, optionally as part of a larger molecule of size at least 6-8 kD.  
CC Where consensus sequence #1 and #2 are: X25X26YG6X1X2X3X4X5N #1,  
CC K6X17X8X9X10X11X12X13X14X15X16X17X18X27X19X20X21X22X23X24Y #2, where  
CC X1, X8, X13 and X24 = L, I or V; X3, X25 and X26 = any amino acid (aa)  
CC or are absent; X27 = L or Y; all other X may be any aa. The peptides  
CC can be used to generate serum antibodies (Ab) that bind at least one  
CC staphylococcal enterotoxin (SE) or streptococcal endotoxin (SPE). Ab  
CC are used: (i) for diagnostic detection of SPEA or SEA, SEB and SED, in  
CC usual immunosays; (ii) to inhibit blastogenesis of human mononuclear  
CC cells in presence of these toxins (i.e. to protect against or alleviate  
CC toxic shock or autoimmune disease associated with bacterial infections);  
CC and (iii) for passive immunisation against effects of the toxins. The  
CC peptides generate Ab that are cross-reactive with toxins from a variety  
CC of bacteria. The present sequence represents a specifically claimed  
CC example of a peptide of the present invention.  
XX  
SQ Sequence 36 AA;  
XX  
QY 1 CMYGGVTLHEGN 12  
DB 1 CMYGGVTLHEGN 12  
XX  
RESULT 10  
AAAY97842  
ID AAY97842 standard; peptide; 36 AA.  
XX  
AC AAY97842;  
XX  
DT 29-AUG-2000 (first entry)  
XX

DE staphylococcal/streptococcal pyrogenic toxin-derived peptide, 6347.  
XX  
KW Pyrogenic exotoxin; enterotoxin; streptococcal infection;  
KW staphylococcal infection; septic shock; toxic shock; vaccine;  
KW antibody.  
XX  
OS Synthetic.  
OS Staphylococcus aureus.  
OS Streptococcus sp. Group A'.  
XX  
PN W0200020598-A1.  
XX  
PD 13-APR-2000.  
XX  
PF 24-SEP-1999; 99WO-US22180.  
XX  
PR 07-OCT-1998; 98US-0168303.  
PR 18-JUN-1999; 99US-0335581.  
XX  
PA (UYRQ ) UNIV ROCKEFELLER.  
XX  
PI Bannan JD, Visvanathan K, Zabriskie JB;  
XX  
PI MPI; 2000-303782/26.  
XX  
PT Peptides useful for preventing and reducing the symptoms of toxic shock  
PT syndrome and septic shock from staphylococcal and streptococcal  
PT infections -  
XX  
PS Claim 4; Page 88; 115pp; English.  
XX  
CC The invention relates to novel peptides (AAY97838-Y97843) comprising a  
CC consensus amino acid sequence derived from two conserved regions  
CC (regions 1 and 2) of Staphylococcus aureus enterotoxins and  
CC streptococcal pyrogenic toxins. Consensus region 1a (a preferred  
CC consensus region 1) has the sequence X25-X26-Y-G-G-X1-T-X2-X3-X4-X5-N  
CC (AAY97863) and consensus region 2a (a preferred consensus region 2) has  
CC the sequence K-X6-X7-X8-  
CC X9-X10-X11-X12-X13-D-X14-X15-X16-R-X17-X18-X27-X19-X20-X21-X22-X23-X24-Y  
CC from L, I and V; X2, X4, X5, X6, X7, X9, X10, X11, X12, X14, X15, X16,  
CC X17, X18, X19, X20, X21, X22 and X23 are each independently selected  
CC the group consisting of any amino acid;  
CC X3, X5 and X26 are each independently selected from the group consisting  
CC of any amino acid and of no amino acid;  
CC X27 is either L or Y.  
CC The invention also relates to serum antibodies induced by the peptides  
CC which provide protection against, or reduce the severity of toxic shock  
CC and septic shock caused by the staphylococcal and streptococcal  
CC pyrogenic toxins. The pyrogenic exotoxins of Group A streptococci and  
CC the enterotoxins of Staphylococcus aureus (which are also pyrogenic  
CC exotoxins) constitute a family of structurally related toxins which  
CC share similar biological activities. They stimulate CD4+ and CD8+ and  
CC gamma-delta+ T-cells by binding the beta-chain variable region (V-beta)  
CC elements on the lateral face of the T-cell receptor (TCR) while  
CC simultaneously binding the lateral face of the class II major  
CC histocompatibility complex (MHC) of antigen presenting cells. This causes  
CC aberrant proliferation of T-cells, which stimulates other components of  
CC the immune system, causing injury to the host. The peptides are used to  
CC prevent, treat or protect against toxic shock and septic shock resulting  
CC from bacterial infections in mammals, particularly humans. The peptides  
CC are used for inducing serum antibodies that bind at least one  
CC staphylococcal enterotoxin or streptococcal exotoxin and both the  
CC peptides and antibodies can be used in diagnostic assays to aid in the  
CC diagnosis of disease related to the presence of bacterial toxins. Nucleic  
CC acids encoding a peptide of the invention can be used for the production  
CC of the peptides for diagnostic reagents, as vaccines and for therapies  
CC for pyrogenic exotoxin related diseases. Vectors expressing high levels  
CC of the peptides can be used in immunotherapy and immunoprophylaxis when  
CC expressed in humans. The antibodies are used for passive immunisation  
CC therapy to prevent or increase resistance to toxic shock syndrome or  
CC septic shock and to ameliorate the effects of conditions associated with  
CC the presence of staphylococcal or streptococcal pyrogenic toxins. The



Db 1 cmvgvtehegn 12

RESULT 13  
AAV97843  
ID AAV97843 standard; peptide: 38 AA.

AC AAV97843:  
29-AUG-2000 (first entry)

DE Staphylococcal/streptococcal pyrogenic toxin-derived peptide, 6348.

XX Pyrogenic exotoxin; enterotoxin; streptococcal infection;  
XX staphylococcal infection; septic shock; toxic shock; vaccine;  
XX antibody.

XX Synthetic.  
OS Staphylococcus aureus.  
OS Streptococcus sp. Group A.

PN WO200020598-A1.  
XX 13-APR-2000.  
XX 24-SEP-1999; 99WO-US22180.  
XX 07-OCT-1998; 98US-0168303.  
PR 18-JUN-1999; 99US-0335581.  
XX (UYRQ ) UNIV ROCKEFELLER.  
XX Bannan JD, Visvanathan K, Zabriskie JB;  
PI WPI: 2000-303782/26.  
DR

PT Peptides useful for preventing and reducing the symptoms of toxic shock  
PT syndrome and septic shock from staphylococcal and streptococcal  
PT infections.

XX Claim 4; Page 88; 115pp; English.

XX The invention relates to novel peptides (AAV97838-Y97843) comprising a  
XX consensus amino acid sequence derived from two conserved regions  
XX (regions 1 and 2) of Staphylococcus aureus enterotoxins and  
XX streptococcal pyrogenic toxins. Consensus region 1a (a preferred  
XX consensus region 1) has the sequence X25-X26-Y-G-G-X1-T-X2-X3-X4-X5-N  
XX (AAV97863) and consensus region 2a (a preferred consensus region 2) has  
XX the sequence K-X6-X7-X8-  
XX X9-X10-X11-X12-X13-D-X14-X15-X16-R-X17-X18-X27-X19-X20-X21-X22-X23-X24-Y  
XX (AAV97864), where: X1, X8, X13 and X24 are each independently selected  
XX from L, I and V; X2, X4, X5, X6, X7, X9, X10, X11, X12, X14, X15, X16,  
XX X17, X18, X19, X20, X21, X22 and X23 are each independently selected from  
XX the group consisting of any amino acid;  
XX X3, X5 and X26 are each independently selected from the group consisting  
XX of any amino acid and of no amino acid;  
XX X27 is either L or Y.

XX The invention also relates to serum antibodies induced by the peptides  
XX which provide protection against, or reduce the severity of toxic shock  
XX and septic shock caused by the staphylococcal and streptococcal  
XX pyrogenic toxins. The pyrogenic exotoxins of Group A streptococci and  
XX the enterotoxins of Staphylococcus aureus (which are also pyrogenic  
XX exotoxins) constitute a family of structurally related toxins which  
XX share similar biological activities. They stimulate CD4+, CD8+ and  
XX gamma-delta+ T-cells by binding the beta-chain variable region (V-beta)  
XX elements on the lateral face of the T-cell receptor (TCR) while  
XX simultaneously binding the lateral face of the class II major  
XX histocompatibility complex (MHC) of antigen presenting cells. This causes  
XX aberrant proliferation of T-cells, which stimulates other components of  
XX the immune system, causing injury to the host. The peptides are used to  
XX prevent, treat or protect against toxic shock and septic shock resulting  
XX from bacterial infections in mammals, particularly humans. The peptides  
XX are used for inducing serum antibodies that bind at least one

CC staphylococcal enterotoxin or streptococcal exotoxin and both the  
CC peptides and antibodies can be used in diagnostic assays to aid in the  
CC diagnosis of disease related to the presence of bacterial toxins. Nucleic  
CC acids encoding a peptide of the invention can be used for the production  
CC of the peptides for diagnostic reagents, as vaccines and for therapies  
CC for pyrogenic exotoxin related diseases. Vectors expressing high levels  
CC of the peptides can be used in immunotherapy and immunoprophylaxis when  
CC expressed in humans. The antibodies are used for passive immunisation  
CC therapy to prevent or increase resistance to toxic shock syndrome or  
CC septic shock and to ameliorate the effects of conditions associated with  
CC the presence of staphylococcal or streptococcal pyrogenic toxins. The  
CC amino acid sequences of the peptides are sufficiently common that they  
CC can be used for eliciting antibodies which are cross-reactive with toxins  
CC derived from various bacteria. Sequences AAV97838-Y97843 represent the  
CC synthetic peptides based on consensus consensus regions 1 and 2 of  
CC Staphylococcus aureus and Group A streptococcal pyrogenic toxins.  
CC These peptides can be administered to a mammal to raise serum antibodies  
CC for protection against or amelioration of toxic or septic shock.

XX Sequence 38 AA;

XX

Query Match 90.1%; Score 64; DB 21; Length 38;  
Best Local Similarity 91.7%; Pred. No. 0.00025;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMVGVTLEHGN 12  
||| ||| ||| |||  
Db 1 cmvgvtehegn 12

RESULT 14  
AAV72181  
ID AAV72181 standard; peptide: 38 AA.

XX 24-APR-2001 (first entry)

DE Peptide #6348, derived from streptococcal and staphylococcal toxins.

XX Mononuclear cell; blastogenesis; inhibitor; HIV; replication; therapy;  
XX staphylococcal enterotoxin; human immunodeficiency virus; T cell;  
XX streptococcal pyrogenic exotoxin; autoimmune disease; immunisation.

OS Streptococcus sp.  
OS Staphylococcus sp.

PN WO200078790-A2.  
XX 28-DEC-2000.  
XX 16-JUN-2000; 2000WO-US16680.  
XX 18-JUN-1999; 99US-0336627.  
XX (UYRQ ) UNIV ROCKEFELLER.  
XX Visvanathan K, Zabriskie JB;  
PI WPI: 2001-080820/09.  
DR

PT Providing protection against, and reducing the severity of, human  
PT immunodeficiency virus infections and associated deleterious effects,  
PT using peptides from homologous sequences of staphylococcal and  
PT streptococcal toxins.

XX Claim 5; Page 38; 76pp; English.

XX The present sequence is peptide #6348, a cross-linked polymer derived  
XX from the homologous sequences of staphylococcal enterotoxin and  
XX streptococcal pyrogenic exotoxin.  
XX The peptide, nucleic acid encoding the peptide and antibody (Ab) produced

CC Against the peptide are useful for inhibiting blastogenesis of  
 CC mononuclear cells (eg. T cells) in the presence of human immunodeficiency  
 CC virus (HIV), inhibiting HIV replication and protecting a mammal against  
 CC the deleterious effects of HIV. The peptide is also used to ameliorate  
 CC the effects of autoimmune diseases associated with the presence of HIV.  
 CC The Ab is used for passively immunising a mammal against the deleterious  
 CC effects of HIV.  
 CC  
 XX

SQ Sequence 38 AA;

Query Match 90.1%; Score 64; DB 22; Length 38;  
 Best Local Similarity 91.7%; Pred. No. 0.00025;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGGVTLHEGN 12  
 ||||| ||||  
 Db 1 cmYggvtehegn 12

RESULT 15

AAR13208 AAR13208 standard; Protein; 238 AA.

AC AAR13208;

DT 15-OCT-1991 (first entry)

DE Staphylococcal enterotoxin C3.

KW SEC3; cancer treatment; pyrogen; tumouricide.

OS Staphylococcus aureus.

PN W09110680-A.

PD 25-JUL-1991.

PF 17-JAN-1991; 91WO-US00342.

PR 17-JAN-1990; 90US-0465577.

PA (TERM/) TERMAN D S.

PI Terman DS;

DR WPI: 1991-237984/32.

PT Treating cancer with enterotoxin from Staphylococcus aureus -  
 PT administered by IV injection, having same tumoricidal activity  
 PT as Staphylococcal protein A without potential toxic reactions

PS Disclosure; Fig 1; 74pp; English.

CC SEC3 was isolated and purified from S.aureus. It can be used for  
 CC treating cancer, activating cytokine mediators and procoagulant  
 CC systems, augmenting natural killer cell cytotoxicity, etc. The  
 CC enterotoxin can be administered intravenously, optionally with  
 CC ibuprofen to attenuate toxic reaction to SEC3. Synthetic  
 CC polypeptides having structural homology to Staphylococcal exotoxins  
 CC are claimed, provided the homology includes statistically  
 CC significant sequence homology, alignment of Cysteine residues and  
 CC similar hydrophathy profiles.  
 CC See AAR13203-R13211.

SQ Sequence 238 AA;

Query Match 90.1%; Score 64; DB 12; Length 238;  
 Best Local Similarity 83.3%; Pred. No. 0.0019;  
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGGVTLHEGN 12

Db 109 cmYggvtehegn 120  
 |||||:| ||||

Search completed: January 2, 2002, 20:48:13  
 Job time: 10129 sec





GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 2, 2002, 20:49:24 ; Search time 56.72 Seconds  
(without alignments)  
16.116 Million cell updates/sec

Title: US-09-335-581A-34  
Perfect score: 71  
Sequence: 1 CMYGGVTLHEGN 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : PIR\_68:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	64	90.1	266	1 ENSAC1	enterotoxin C-1 pr
2	64	90.1	266	2 A60114	enterotoxin C-2 pr
3	64	90.1	266	3 S11885	enterotoxin C3 - S
4	62	87.3	257	2 A28664	enterotoxin A prec
5	62	87.3	257	2 A28179	enterotoxin B prec
6	61	85.9	250	1 A26152	streptococcal pyro
7	60	84.5	236	2 S18789	exotoxin A precurs
8	60	84.5	236	2 S18786	exotoxin type A pr
9	60	84.5	236	2 S18783	exotoxin type A pr
10	60	84.5	251	1 S29659	exotoxin type A pr
11	59	83.1	266	1 ENSAB6	enterotoxin B prec
12	58	81.7	258	2 A33953	enterotoxin D prec
13	43	60.6	841	2 J00647	preprotein translo
14	42	59.2	270	2 B48826	high choriolytic h
15	42	59.2	279	2 C48826	high choriolytic h
16	42	59.2	895	2 T11979	preprotein translo
17	41.5	58.5	463	2 A38463	fibritogen beta ch
18	41	57.7	185	2 S04792	mobilization prote
19	41	57.7	437	2 S69881	phosphorylase hy
20	41	57.7	437	2 S67305	phosphorylase hy
21	40	56.3	810	2 T10736	Nel-homolog protei
22	40	56.3	968	2 A37867	transcription fact
23	39	54.9	156	2 B83855	transposase (09) B
24	39	54.9	156	2 G83886	transposase (09) B
25	39	54.9	156	2 B84005	transposase (09) B
26	39	54.9	156	2 B84005	transposase (09) B
27	39	54.9	156	2 B84034	transposase (09) B
28	39	54.9	156	2 B84083	transposase (09) B
29	39	54.9	156	2 F84084	transposase (09) B

30	39	54.9	156	2 H83671	transposase (09) B
31	39	54.9	156	2 E83683	transposase (09) B
32	39	54.9	198	2 S54733	ribosomal protein
33	39	54.9	767	2 A35645	major surface prot
34	39	54.9	805	2 T40739	rm3-pil1 helicase
35	39	54.9	805	2 T47241	RMH3/Pil1 helicase
36	39	54.9	916	2 D83093	secretion protein
37	38	53.5	265	2 S38380	Hroxl protein - Ca
38	38	53.5	347	2 T26349	hypothetical prote
39	38	53.5	347	2 T35013	probable membrane
40	38	53.5	813	2 T40622	translation elonga
41	38	53.5	871	2 C72238	preprotein translo
42	38	53.5	1028	2 E85089	probable transposo
43	37	52.1	159	2 T30926	hypothetical prote
44	37	52.1	284	2 H84124	3-hydroxybutyryl-C
45	37	52.1	295	2 C83244	conserved hypothet

## ALIGNMENTS

```
RESULT 1
ENSAC1
enterotoxin C-1 precursor - Staphylococcus aureus
C:Species: Staphylococcus aureus
C>Date: 15-Nov-1984 #sequence_revision 05-Jan-1996 #text_change 18-Jun-1999
C:Accession: S06356; A01816
R:Bohach, G.A.; Schlievert, P.M.
Mol. Gen. Genet. 209, 15-20, 1987
A>Title: Nucleotide sequence of the staphylococcal enterotoxin CI gene and relatedness
A:Reference number: S06356; MUID:88038352
A:Accession: S06356
A:Molecule type: DNA
A:Residues: 1266 <BOH>
A:Cross-references: EMBL:X05815; NID:946566; PIDN:CAA29260.1; PID:946567
R:Schmidt, J.J.; Spero, L.
J. Biol. Chem. 258, 6300-6306, 1983
A>Title: The complete amino acid sequence of Staphylococcal enterotoxin C-1.
A:Reference number: A01816; MUID:83213327
A:Accession: A01816
A:Molecule type: Protein
A:Residues: 28-75, 'IL', 78-176, 'N', 178-266 <SCH>
C:Gene: entC1
C:Superfamily: enterotoxin B
C:Keywords: enterotoxin
F:1-27/Domain: signal sequence #status predicted <SIG>
F:28-266/Product: enterotoxin C-1 #status experimental <MAT>
F:120-137/Disulfide bonds: #status experimental

Query Match          90.1%   Score 64: DB 1: Length 266;
Best Local Similarity 83.3%: Pred. No. 0.00091;
Matches 10: Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

QY 1 CMYGGVTLHEGN 12  
DB 137 CMYGGVTLHEGN 148

RESULT 2  
A60114  
enterotoxin C-2 precursor - Staphylococcus aureus  
N:Alternate names: enterotoxin C-3 precursor  
C:Species: Staphylococcus aureus  
C>Date: 10-Nov-1992 #sequence\_revision 10-Nov-1992 #text\_change 16-Jul-1999  
C:Accession: A60114; B60114; A33866  
R:Bohach, G.A.; Schlievert, P.M.  
Infect. Immun. 57, 2249-2252, 1989  
A>Title: Conservation of the biologically active portions of staphylococcal enterotox  
A:Reference number: A60114; MUID:85277549  
A:Accession: A60114  
A>Status: not compared with conceptual translation

A:Molecule type: DNA  
A:Residues: 1-266 <BOH>  
A:Accession: B60114  
A:Molecule type: protein  
A:Residues: 28-66 <BOH2>  
R:Couch, J.L.; Betley, M.J.  
J. Bacteriol. 171, 4507-4510, 1989  
A:Title: Nucleotide sequence of the type C-3 staphylococcal enterotoxin gene suggests th  
A:Reference number: A33866; MUID:89327174  
A:Accession: A33866  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-266 <COU>  
A:Cross-references: GB:M28364; NID:g153003; PIDN:AAA26624.1; PID:g153004  
C:Genetics:  
A:Gene: entC2  
C:Superfamily: enterotoxin B  
F:1-27/Domain: signal sequence #status predicted <SIG>  
F:28-266/Product: enterotoxin C-2 #status predicted <MAT>

Query Match 90.1%; Score 64; DB 2; Length 266;  
Best Local Similarity 83.3%; Pred. No. 0.00091;  
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGVTLHEGN 12  
|||||:|||||  
DB 137 CMYGVTLHEGN 148

RESULT 3  
S11885  
enterotoxin C3 - Staphylococcus aureus  
C:Species: Staphylococcus aureus  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 16-Jul-1999  
C:Accession: S11885  
R:Howe, C.J.; Hackett, S.P.; Bohach, G.A.  
Mol. Gen. Genet. 220, 329-333, 1990  
A:Title: Nucleotide sequence of the staphylococcal enterotoxin C3 gene: sequence compar  
A:Reference number: S11885; MUID:90220508  
A:Accession: S11885  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-266 <HOV>  
A:Cross-references: GB:X51661; NID:g46570; PIDN:CAA35972.1; PID:g46571  
C:Superfamily: enterotoxin B

Query Match 90.1%; Score 64; DB 2; Length 266;  
Best Local Similarity 83.3%; Pred. No. 0.00091;  
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGVTLHEGN 12  
|||||:|||||  
DB 137 CMYGVTLHEGN 148

RESULT 4  
A28664  
enterotoxin A precursor - Staphylococcus aureus  
C:Species: Staphylococcus aureus  
C:Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 15-Oct-1999  
C:Accession: A28664; A29566  
R:Betley, M.J.; Mekalanos, J.J.  
J. Bacteriol. 170, 34-41, 1988  
A:Title: Nucleotide sequence of the type A staphylococcal enterotoxin gene.  
A:Reference number: A28664; MUID:8806892  
A:Accession: A28664  
A:Molecule type: DNA  
A:Residues: 1-257 <BET>  
A:Cross-references: GB:M18970; NID:g153120; PIDN:AAA26681.1; PID:g153121  
A:Experimental source: strain FRI337  
R:Huang, I.Y.; Hughes, J.L.; Bergdoll, M.S.; Schantz, E.J.

J. Biol. Chem. 262, 7006-7013, 1987  
A:Title: Complete amino acid sequence of staphylococcal enterotoxin A.  
A:Reference number: A29566; MUID:87222293  
A:Accession: A29566  
A:Molecule type: protein  
A:Residues: 25-241, 'S', 243-257 <HUA>  
C:Genetics:  
A:Gene: entA  
A:Map position: 6  
C:Superfamily: enterotoxin B

Query Match 87.3%; Score 62; DB 2; Length 257;  
Best Local Similarity 83.3%; Pred. No. 0.002;  
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGVTLHEGN 12  
|||||:|||||  
DB 130 CMYGVTLHDNN 141

RESULT 5  
A28179  
enterotoxin E precursor - Staphylococcus aureus  
C:Species: Staphylococcus aureus  
C:Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 15-Oct-1999  
C:Accession: A28179  
R:Couch, J.L.; Solits, M.T.; Betley, M.J.  
J. Bacteriol. 170, 2954-2960, 1988  
A:Title: Cloning and nucleotide sequence of the type E staphylococcal enterotoxin gen  
A:Reference number: A28179; MUID:88257005  
A:Accession: A28179  
A:Molecule type: DNA  
A:Residues: 1-257 <COU>  
A:Cross-references: GB:M21319; NID:g153001; PIDN:AAA26617.1; PID:g153002  
C:Superfamily: enterotoxin B

Query Match 87.3%; Score 62; DB 2; Length 257;  
Best Local Similarity 83.3%; Pred. No. 0.002;  
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGVTLHEGN 12  
|||||:|||||  
DB 130 CMYGVTLHDNN 141

RESULT 6  
A26152  
streptococcal pyrogenic exotoxin type A precursor - Streptococcus sp.  
N:Alternate names: scarlet fever toxin; SPE type A (speA)  
C:Species: Streptococcus sp.  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: A26152  
R:Johnson, L.P.; L'Italien, J.J.; Schlievert, P.M.  
Mol. Gen. Genet. 203, 354-356, 1986  
A:Title: Streptococcal pyrogenic exotoxin type A (scarlet fever toxin) is related to  
A:Reference number: A26152; MUID:86284313  
A:Accession: A26152  
A:Molecule type: DNA  
A:Residues: 1-250 <JOH>  
C:Superfamily: enterotoxin B  
C:Keywords: exotoxin

Query Match 85.9%; Score 61; DB 1; Length 250;  
Best Local Similarity 83.3%; Pred. No. 0.002;  
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGVTLHEGN 12  
|||||:|||||  
DB 128 CMYGVTLHEGN 139

```
RESULT 7
S18789
exotoxin A precursor (allele 4) - Streptococcus pyogenes (strain MGAS252 isolate Califor
N:Alternate names: scarlet fever toxin
C:Species: Streptococcus pyogenes
A:Variety: strain MGAS252 isolate California
C:Date: 29-Jan-1993 #sequence_rev:150 #text_change:16-Jul-1999
R:Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
J. Exp. Med. 174, 1271-1274, 1991
A:Title: Characterization and clonal distribution of four alleles of the speA gene encod
A:Reference number: S18782; MUID:92044323
A:Accession: S18789
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEZ>
A:Cross-references: EMBL:X61573; NID:q47303; PIDN:CAA43771.1; PID:q47304
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
C:Genetics:
A:Gene: speA
C:Superfamily: enterotoxin B
C:Keywords: exotoxin
F:1-22/Domain: signal sequence (fragment) #status predicted <SIG>
F:23-236/Product: exotoxin A (fragment) #status predicted <MAT>

Query Match 84.5% Score 60; DB 2; Length 236;
Best Local Similarity 83.3% Pred. No. 0.0041;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 CMYGVTLHEGN 12
|:||||| |||
Db 120 CTVGVTHNHCN 131

RESULT 8
S18786
exotoxin type A precursor (allele 2) - Streptococcus pyogenes phage (strain MGAS250 isol
N:Alternate names: scarlet fever toxin
C:Species: Streptococcus pyogenes phage
A:Variety: strain MGAS250 isolate California; strain MGAS251 isolate California; strain
Isolate United Kingdom; strain MGAS496 isolate Germany
C:Date: 29-Jan-1993 #sequence_rev:150 #text_change:16-Jul-1999
R:Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
J. Exp. Med. 174, 1271-1274, 1991
A:Title: Characterization and clonal distribution of four alleles of the speA gene encod
A:Reference number: S18782; MUID:92044323
A:Accession: S18786
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEZ>
A:Cross-references: EMBL:X61561; NID:q47297; PIDN:CAA43759.1; PID:q47298
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18787
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEA>
A:Cross-references: EMBL:X61562; NID:q47299; PIDN:CAA43760.1; PID:q47300
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18788
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEZ>
A:Cross-references: EMBL:X61563; NID:q47301; PIDN:CAA43761.1; PID:q47302
A:Experimental source: strain MGAS256 isolate California unassigned phage
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18790
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
```

```
A:Residues: 1-236 <NEV>
A:Cross-references: EMBL:X61564; NID:q47305; PIDN:CAA43762.1; PID:q47306
A:Experimental source: strain MGAS285 isolate Colorado unassigned phage
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199
A:Accession: S18792
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEO>
A:Cross-references: EMBL:X61565; NID:q47311; PIDN:CAA43763.1; PID:q47312
A:Experimental source: strain MGAS480 isolate Yugoslavia unassigned phage
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199
A:Accession: S18795
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEH>
A:Cross-references: EMBL:X61566; NID:q47317; PIDN:CAA43764.1; PID:q47318
A:Experimental source: strain MGAS492 isolate United Kingdom unassigned phage
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199
A:Accession: S18799
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NES>
A:Cross-references: EMBL:X61567; NID:q47325; PIDN:CAA43765.1; PID:q47326
A:Experimental source: strain MGAS496 isolate Germany unassigned phage
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199
C:Genetics:
A:Gene: speA2
C:Superfamily: enterotoxin B
C:Keywords: exotoxin
F:1-22/Domain: signal sequence (fragment) #status predicted <SIG>
F:23-236/Product: exotoxin type A (fragment) #status predicted <MAT>

Query Match 84.5% Score 60; DB 2; Length 236;
Best Local Similarity 83.3% Pred. No. 0.0041;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 CMYGVTLHEGN 12
|:||||| |||
Db 120 CTVGVTHNHCN 131

RESULT 9
S18783
exotoxin type A precursor (allele 3) - Streptococcus pyogenes phage (strain MGAS158 i
N:Alternate names: scarlet fever toxin
C:Species: Streptococcus pyogenes phage
A:Variety: strain MGAS158 isolate Nebraska; strain MGAS485 isolate Yugoslavia; strain
C:Date: 29-Jan-1993 #sequence_rev:150 #text_change:16-Jul-1999
R:Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
J. Exp. Med. 174, 1271-1274, 1991
A:Title: Characterization and clonal distribution of four alleles of the speA gene en
A:Reference number: S18782; MUID:92044323
A:Accession: S18783
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEZ>
A:Cross-references: EMBL:X61568; NID:q47289; PIDN:CAA43766.1; PID:q47290
A:Experimental source: strain MGAS158 isolate Nebraska unassigned phage
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199
A:Accession: S18793
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEA>
A:Cross-references: EMBL:X61569; NID:q47313; PIDN:CAA43767.1; PID:q47314
A:Experimental source: strain MGAS485 isolate Yugoslavia unassigned phage
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199
A:Accession: S18794
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEZ>
A:Cross-references: EMBL:X61570; NID:q47315; PIDN:CAA43768.1; PID:q47316
```

A:Experimental source: strain MGAS491 isolate United Kingdom unassigned phage  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991  
A:Accession: S18801  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-236 <MEY>  
A:Cross-references: EMBL:X61572; NID:g47333; PIDN:CAA43770.1; PID:g47334  
A:Experimental source: strain MGAS624 isolate Germany unassigned phage  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991  
A:Accession: S18798  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-236 <NEO>  
A:Cross-references: EMBL:X61571; NID:g47323; PIDN:CAA43769.1; PID:g47324  
A:Experimental source: strain MGAS495 isolate Germany unassigned phage  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991  
C:Genetics:  
A:Gene: speA3  
C:Superfamily: enterotoxin B  
C:Keywords: exotoxin  
F:1-22/Domain: signal sequence (fragment) #status predicted <SIG>  
F:23-236/Product: exotoxin type A (fragment) #status predicted <MAT>

Query Match 84.5%; Score 60; DB 2; Length 236;  
Best local similarity 83.3%; Pred. No. 0.0041;  
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGVTLHEGN 12  
Db 120 CIXGVTHNHCN 131

RESULT 10  
S29659  
exotoxin type A precursor (allele 1) - Streptococcus pyogenes phage T12

M:Alternate names: erythrogenic toxin; scarlet fever toxin  
C:Species: Streptococcus pyogenes phage T12

C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999

C:Accession: S29659; S18782; S18784; S18785; S18791; S18796; S18797; S18800

R:Weeks, C.R.; Perrett, J.J.

Infect. Immun. 57, 144-150, 1986

A:Title: Nucleotide sequence of the type A streptococcal exotoxin (erythrogenic toxin) g

A:Reference number: S29659; MOID:8616804

A:Accession: S29659

A:Molecule type: DNA

A:Residues: 1-251 <MEB>  
A:Cross-references: GB:U04053; EMBL:M19350; NID:g1877426; PIDN:AA048686.1; PID:g1877430

R:Welson, K.; Schliefert, P.M.; Selander, R.K.; Musser, J.M.

J. Exp. Med. 174, 1271-1274, 1991  
A:Title: Characterization and clonal distribution of four alleles of the speA gene encod

A:Reference number: S18782; MOID:92044323

A:Accession: S18782

A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA

A:Residues: 9-244 <NEA>

A:Cross-references: EMBL:X61560; NID:g47287; PIDN:CAA43758.1; PID:g47288  
A:Experimental source: Streptococcus pyogenes strain MGAS156 isolate Nebraska unassigned

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991  
A:Accession: S18784

A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA

A:Residues: 9-244 <NEA>  
A:Cross-references: EMBL:X61556; NID:g47291; PIDN:CAA43754.1; PID:g47292

A:Experimental source: Streptococcus pyogenes strain MGAS165 isolate Minnesota unassigned

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991  
A:Accession: S18785

A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA

A:Residues: 9-244 <NEZ>

A:Cross-references: EMBL:X61559; NID:g47293; PIDN:CAA43757.1; PID:g47294  
A:Experimental source: Streptococcus pyogenes strain MGAS167 isolate Texas unassigned ph

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991

A:Accession: S18791  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 9-244 <MEY>  
A:Cross-references: EMBL:X61555; NID:g47309; PIDN:CAA43753.1; PID:g47310  
A:Experimental source: Streptococcus pyogenes strain MGAS327 isolate Arizona unassign  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199  
A:Accession: S18796  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 9-244 <NEO>  
A:Cross-references: EMBL:X61557; NID:g47319; PIDN:CAA43755.1; PID:g47320  
A:Experimental source: Streptococcus pyogenes strain MGAS493 isolate France unassigned  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199  
A:Accession: S18797  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 9-244 <MEB>  
A:Cross-references: EMBL:X61558; NID:g47321; PIDN:CAA43756.1; PID:g47322  
A:Experimental source: Streptococcus pyogenes strain MGAS494 isolate France unassigned  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199  
A:Accession: S18800  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 9-228 <NES>  
A:Cross-references: EMBL:X61554; NID:g47327; PIDN:CAA43752.1; PID:g47328  
A:Experimental source: Streptococcus pyogenes strain MGAS500 isolate New Zealand unassigned  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199  
C:Genetics:  
A:Gene: speA1  
C:Superfamily: enterotoxin B  
C:Keywords: exotoxin  
F:1-30/Domain: signal sequence #status predicted <SIG>  
F:31-251/Product: exotoxin type A #status predicted <MAT>

Query Match 84.5%; Score 60; DB 1; Length 251;  
Best local similarity 83.3%; Pred. No. 0.0043;  
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGVTLHEGN 12  
Db 128 CIXGVTHNHCN 139

RESULT 11  
ENSAB6

enterotoxin B precursor - Staphylococcus aureus

C:Species: Staphylococcus aureus

C:Date: 24-Apr-1984 #sequence\_revision 15-Oct-1996 #text\_change 18-Jun-1999

C:Accession: S27360; A92065; S27240; A01815

R:Jones, C.L.; Khan, S.A.

J. Bacteriol. 166, 29-33, 1986  
A:Title: Nucleotide sequence of the enterotoxin B gene from Staphylococcus aureus.

A:Reference number: S27360; MOID:86168029

A:Accession: S27360  
A:Molecule type: DNA

A:Residues: 1-266 <RON>

A:Cross-references: EMBL:M11118; NID:g152999; PIDN:AAA86550.1; PID:g153000  
A:Experimental source: strain S6

R:Huang, I.Y.; Bergdoll, M.S.

J. Biol. Chem. 245, 3518-3525, 1970

A:Title: The primary structure of staphylococcal enterotoxin B. III. The cyanogen bro  
A:Reference number: A92065; MOID:71007902

A:Accession: A92065

A:Molecule type: protein  
A:Residues: 28-55, 'NND', '59-68', 'NE', '71', 'FDLYL', '78-117', '119-127', 'N', '129', 'D', '131-132', 'EN

A:Experimental source: strain S-6  
R:Huang, I.Y.; Bergdoll, M.S.

J. Biol. Chem. 245, 3511-3517, 1970  
A:Title: The primary structure of staphylococcal enterotoxin B. II. Isolation, compos

A:Reference number: A92064; MOID:71007901

A:Contents: annotation; chymotryptic peptides

R: Huang, I. Y.; Bergdoll, M. S.  
 J. Biol. Chem. 245, 3493-3510, 1970  
 A: Title: The primary structure of staphylococcal enterotoxin B. I. Isolation, composition  
 A: Reference number: A92063; MUID: 71007900  
 A: Contents: annotation; tryptic peptides  
 R: Schantz, E. J.; Roessler, W. G.; Wagnan, J.; Spero, L.; Dunmery, D. A.; Bergdoll, M. S.  
 Biochemistry 4, 1011-1016, 1965  
 A: Title: Purification of staphylococcal enterotoxin B.  
 A: Reference number: A90548; MUID: 66035792  
 A: Contents: annotation; biological source of protein  
 R: Alakhov, V. Y.; Klinsky, E. Y.; Kolosov, M. I.; Maurer-Fogy, I.; Moskaleva, E. Y.; Sveshnik  
 Eur. J. Biochem. 209, 823-828, 1992  
 A: Title: Identification of functionally active fragments of staphylococcal enterotoxin B  
 A: Reference number: S27240; MUID: 93049338  
 A: Accession: S27240  
 A: Molecule type: protein  
 A: Residues: 28-42:128-148 <ALA>  
 C: Superfamily: enterotoxin B  
 C: Keywords: enterotoxin; extracellular protein; toxin  
 F: 1-27/Domain: signal sequence #status predicted <SIG>  
 F: 28-266/Product: enterotoxin B #status experimental <MAT>  
 F: 120-140/Disulfide bonds: #status experimental

Query Match 83.1%; Score 59; DB 1; Length 266;  
 Best Local Similarity 83.3%; Pred. No. 0.0068;  
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CMYGVTLHEGN 12  
 ||||| | |  
 Db 140 CMYGVTEHNGN 151

RESULT 12  
 A33953  
 enterotoxin D precursor - Staphylococcus aureus  
 C: Species: Staphylococcus aureus  
 C: Date: 09-Mar-1990 #sequence\_revision 09-Mar-1990 #text\_change 15-Oct-1999  
 C: Accession: A33953  
 R: Bayles, K. W.; Iandolo, J. J.  
 J. Bacteriol. 171, 4799-4806, 1989  
 A: Title: Genetic and molecular analyses of the gene encoding staphylococcal enterotoxin  
 A: Reference number: A33953; MUID: 69359112  
 A: Accession: A33953  
 A: Status: preliminary  
 A: Molecule type: DNA  
 A: Residues: 1-258 <BAV>  
 A: Cross-references: GB:M28521; NID:g1492109; PIDN:AAB06195.1; PID:g758691  
 C: Superfamily: enterotoxin B

Query Match 81.7%; Score 58; DB 2; Length 258;  
 Best Local Similarity 83.3%; Pred. No. 0.01;  
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CMYGVTLHEGN 12  
 ||||| | |  
 Db 131 CTVGVTPHEGN 142

RESULT 13  
 J00647  
 preprotein translocase secA - Bacillus subtilis  
 N: Alternate names: Div protein; secA protein homolog  
 C: Species: Bacillus subtilis  
 C: Date: 04-Dec-1992 #sequence\_revision 04-Dec-1992 #text\_change 17-Nov-2000  
 C: Accession: J00647; S17771; F69704  
 R: Sedate, Y.; Takematsu, H.; Nakamura, K.; Yamane, K.  
 Gene 98, 101-105, 1991  
 A: Title: Sequencing reveals similarity of the wild-type div+ gene of Bacillus subtilis  
 A: Reference number: JN0145; MUID: 91192600  
 A: Accession: J00647  
 A: Molecule type: DNA

A: Residues: 1-841 <SAD>  
 A: Cross-references: GB:D10279; DDBJ:D90218; NID:g216332; PIDN:BAA01122.1; PID:g216334  
 A: Experimental source: strain Marburg 168T  
 R: Overhoff, B.; Klein, M.; Spies, M.; Freudl, R.  
 Mol. Gen. Genet. 228, 417-423, 1991  
 A: Title: Identification of a gene fragment which codes for the 364 amino-terminal and  
 export apparatus in gram-positive and gram-negative bacteria.  
 A: Reference number: S17771; MUID: 91375427  
 A: Accession: S17771  
 A: Molecule type: DNA  
 A: Residues: 1-125, 127-364 <OVE>  
 A: Cross-references: EMBL:X62035; NID:g48979; PIDN:CAA43977.1; PID:g48980  
 R: Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A. M.; Alloni, G.; Azevedo, V.; Ber  
 C.; Bron, S.; Brouillet, S.; Bruschi, C. V.; Caldwell, B.; Capuano, V.; Carter, N. M.;  
 A.; Ehrlich, S. D.; Emmerzon, P. T.; Entian, K. D.; Errington, J.; Fabel, C.; Ferrari,  
 Nature 390, 249-256, 1997  
 A: Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gal  
 lech, J.; Harwood, C. R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M  
 Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino  
 A: Authors: Lauber, J.; Lazarevic, V.; Lee, S. M.; Levine, A.; Liu, H.; Masuda, S.; Mau  
 Y, M.; Ogawa, K.; Ogihara, A.; Oudega, B.; Park, S. H.; Parro, V.; Pohl, T. M.; Potte  
 Rieger, M.; Rivolta, C.; Roche, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanl  
 A: Authors: Schleicher, S.; Schreier, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se  
 akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terstara, P.; Tognoni, A.; Tosato, V.; Uchiya  
 T.; Winters, P.; Wipet, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yeta, K.; Yoshida  
 A: Authors: Yoshikawa, H. F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.  
 A: Title: The complete genome sequence of the gram-positive bacterium Bacillus subtilis  
 A: Reference number: A69580; MUID: 98044033  
 A: Accession: F69704  
 A: Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A: Molecule type: DNA  
 A: Residues: 1-841 <KUN>  
 A: Cross-references: GB:299122; GB:AL009126; NID:g2636029; PIDN:CAB15547.1; PID:g26360  
 A: Experimental source: strain 168  
 C: Comment: This pleiotropic protein is required for cell division, sporulation, septa  
 C: Comment: The "nucleotide-binding motif B" and "DAD motif" features as annotated ar  
 C: Genetics: is adjacent to the identified motif and a third conserved motif is approximately 120-1  
 C: Gene: secA; div  
 C: Superfamily: preprotein translocase secA  
 C: Keywords: ATP; membrane-associated complex; P-loop; protein transport; sporulation  
 F: 100-107/Region: nucleotide-binding motif A (P-loop) #status atypical  
 F: 203-208/Region: nucleotide-binding motif B  
 F: 207-210/Region: DEXH motif

Query Match 60.6%; Score 43; DB 2; Length 841;  
 Best Local Similarity 63.6%; Pred. No. 14;  
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 MYGVTLHEGN 12  
 : ||| || |  
 Db 86 IMGVALLHDGN 96

RESULT 14  
 B48826  
 high chorolytic hatching proteinase (EC 3.4.24.-) HCE23 precursor - Japanese medaka  
 C: Species: Oryzias latipes (Japanese medaka)  
 C: Date: 01-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 21-Jul-2000  
 C: Accession: B48826  
 R: Yasumasa, S.; Yamada, K.; Akasaka, K.; Mitsunaga, K.; Iuchi, I.; Shinada, H.; Yamag  
 Dev. Biol. 153, 250-258, 1992  
 A: Title: Isolation of cDNAs for LCE and HCE, two constituent proteases of the hatchin  
 A: Reference number: A48826; MUID: 93012471  
 A: Accession: B48826  
 A: Molecule type: mRNA; protein  
 A: Residues: 1-270 <YAS>  
 A: Cross-references: GB:M96170; NID:g213501; PIDN:AAA49438.1; PID:g213502  
 A: Experimental source: orange red variety, embryo  
 A: Note: sequence extracted from NCBI backbone (NCBIN:114769, NCBI:114770)  
 C: Superfamily: astacin; astacin homology

C:Keywords: glycoprotein; hydrolase; metalloproteinase; zinc  
 F:1-20/Domain: signal sequence #status predicted <SIG>  
 F:21-70/Domain: propeptide #status predicted <PRO>  
 F:71-270/Product: low choriolytic hatching proteinase #status predicted <MAT>  
 F:88-270/Domain: astacin homology <AST>  
 F:53/Binding site: carbohydrate (asn) (covalent) #status predicted  
 F:169,173,179,225/Binding site: zinc (His, His, His, Tyr) #status predicted  
 F:170/Active site: Glu #status predicted

Query Match 59.2%; Score 42; DB 2; Length 270;  
 Best Local Similarity 58.3%; Pred. No. 6.7;

Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CMYGGVTLHEGN 12  
 ||| | : || |  
 Db 161 CMYSGIIQHELN 172

## RESULT 15

C48826 high choriolytic hatching proteinase (EC 3.4.24.-) HCE21 precursor - Japanese medaka  
 C:Species: Oryzias latipes (Japanese medaka)  
 C:Date: 08-Feb-1996 #sequence\_revision 08-Feb-1996 #text\_change 03-Dec-1999  
 C:Accession: C48826  
 R:Yasumasu, S.; Yamada, K.; Akasaka, K.; Mitsunaga, K.; Iuchi, I.; Shimada, H.; Yamagami, Dev. Biol. 153, 250-258, 1992  
 A:Title: Isolation of cDNAs for LCE and HCE, two constituent proteases of the hatching e  
 A:Reference number: A48826; MUID:93012471  
 A:Accession: C48826  
 A:Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-279 <YAS>  
 A:Cross-references: GB:M96171  
 C:Superfamily: astacin; hydrolase; metalloproteinase; zinc  
 C:Keywords: glycoprotein; signal sequence #status predicted <SIG>  
 F:1-20/Domain: signal sequence #status predicted <PRO>  
 F:21-79/Domain: propeptide #status predicted <MAT>  
 F:80-279/Product: low choriolytic hatching proteinase #status predicted <MAT>  
 F:97-279/Domain: astacin homology <AST>  
 F:62/Binding site: carbohydrate (asn) (covalent) #status predicted  
 F:178,182,188,234/Binding site: zinc (His, His, His, Tyr) #status predicted  
 F:179/Active site: Glu #status predicted

Query Match 59.2%; Score 42; DB 2; Length 279;  
 Best Local Similarity 58.3%; Pred. No. 7;

Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CMYGGVTLHEGN 12  
 ||| | : || |  
 Db 170 CMYSGIIQHELN 181

Search completed: January 2, 2002, 20:49:25  
 Job time: 785 sec

GenCore version 4.5  
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## OM protein - protein search, using sw model

Run on: January 2, 2002, 20:50:15 ; Search time 37.4 Seconds  
(Without alignments)  
11.764 Million cell updates/sec

Title: US-09-335-581a-34

Sequence: 1 CMYGGVTLHEGN 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	64	90.1	266	ETC1_STAU	P01553 staphylococ
2	64	90.1	266	ETC2_STAU	P34071 staphylococ
3	64	90.1	266	ETC3_STAU	P23313 staphylococ
4	62	87.3	257	ETXA_STAU	P13163 staphylococ
5	62	87.3	257	ETXE_STAU	P12993 staphylococ
6	60	84.5	251	SPEA_STRPY	P08095 streptococ
7	59	83.1	266	ETXB_STAU	P01552 staphylococ
8	58	81.7	258	ETXD_STAU	P20723 staphylococ
9	43	60.6	841	SECA_BACSU	P28366 bacillus su
10	42	59.2	270	HCE1_ORYLA	P31580 oryztias lat
11	42	59.2	279	HCE2_ORYLA	P31581 oryztias lat
12	42	59.2	895	SECA_CVACA	O19911 cyandium c
13	41.5	58.5	463	FIBB_CHICK	Q02020 gallus galli
14	41.5	57.7	437	ERR1_YEAST	P42222 saccharomyc
15	40	56.3	810	NEL1_HUMAN	Q02812 homo sapien
16	40	56.3	810	NEL1_RAT	Q02919 rattus norv
17	40	56.3	904	SECA_RHOCA	P32966 rhodobacter
18	40	56.3	969	KBF1_HUMAN	P19838 homo sapien
19	40	56.3	971	KBF1_MOUSE	P25799 mus musculu
20	39	54.9	170	R57_DESMO	P41206 desulfuroc
21	39	54.9	805	PIE1_SCHPO	Q09422 schistosach
22	38	53.5	413	HEMO_MANSE	P31398 manduca sex
23	38	53.5	836	SECA_LISMO	P47847 listeria mo
24	37	52.1	869	YO27_BPHPI	P51731 bacterioph
25	37	52.1	984	SECA_AQUAE	O67718 aquifex aeo
26	36	50.7	115	GUAN_HUAE	Q02747 homo sapien
27	36	50.7	128	YF75_MYCPN	P75204 mycoplasma
28	36	50.7	281	W125_MYCPN	P75204 mycoplasma
29	36	50.7	289	ISPE_BACSU	P37550 bacillus su
30	36	50.7	455	YSD1_CAEEL	P48459 caenorhabdi
31	36	50.7	857	PIF1_YEAST	P07271 saccharomyc
32	36	50.7	948	SECA_SYNP7	Q53357 synecococc
33	36	50.7	1021	Y2R2_DROME	P16425 drosophila

## ALIGNMENTS

34	35	49.3	139	1	YBPE_BURCE	P37336 burkholderi
35	35	49.3	149	1	YKKA_YEAST	P42949 saccharomyc
36	35	49.3	191	1	SPR6_YEAST	Q01684 saccharomyc
37	35	49.3	251	1	ASTA_ASTFL	P07584 astacus flu
38	35	49.3	315	1	PHSS_DESBA	P13063 desulfovibr
39	35	49.3	352	1	THRC_BACSU	P04990 bacillus su
40	35	49.3	367	1	FIIBP_ADEL15	P36847 human adeno
41	35	49.3	432	1	WISA_YEAST	P40564 saccharomyc
42	35	49.3	564	1	YKK9_CAEEL	P34286 caenorhabdi
43	35	49.3	574	1	GAL2_YEAST	P13181 saccharomyc
44	35	49.3	700	1	TOP1_CAMJE	O9P122 campylobact
45	35	49.3	742	1	SVV2_RAT	Q02563 rattus norv

RESULT 1  
ETC1\_STAU STANDARD: PRT: 266 AA.  
ID ETC1\_STAU  
AC P01553;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-JAN-1990 (Rel. 13, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE ENTEROTOXIN TYPE C-1 PRECURSOR (SEC1).  
GN ETC1.  
OS Staphylococcus aureus.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
OC Bacillus/Staphylococcus group; Staphylococcus.  
OX NCBI\_TaxId=1280;  
[1]  
RN SEQUENCE FROM N.A.  
RX MEDLINE=88038352; PubMed=2823067;  
RA Bohach G.A., Schlievert P.M.;  
RT "Nucleotide sequence of the staphylococcal enterotoxin C1 gene and  
RT relatedness to other pyrogenic toxins.";  
RL Mol. Gen. Genet. 209:15-20(1987).  
[2]  
RN SEQUENCE OF 28-266.  
RX MEDLINE=83213327; PubMed=6189824;  
RA Schmidt J.J., Spero L.;  
RT "The complete amino acid sequence of staphylococcal enterotoxin C1.";  
RL J. Biol. Chem. 258:6300-6306(1983).  
CC -I- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION  
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.  
CC -I- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES  
CC PYROGENIC EXOTOXINS ARE ALL RELATED.  
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-----  
CC EMBL: X05815; CA29260.1; -;  
DR PIR: A01816; ENSAC1.  
DR PIR: S06356; S06356.  
DR HSSP: P34071; ISE2.  
DR InterPro: IPR001961; Staph.Strep.toxin.  
DR Pfam: PF01123; Staph.Strep.toxin.  
DR PRINTS: PR00279; BACTRTOXIN.  
DR PROSITE: PS00277; STAPH\_STREP\_TOXIN\_1; 1.  
DR PROSITE: PS00278; STAPH\_STREP\_TOXIN\_2; 1.  
KW Enterotoxin; Toxin; Signal; Superantigen.  
FT SIGNAL 1 27  
FT CHAIN 28 266 ENTEROTOXIN TYPE C-1.  
FT DISULFID 120 137  
FT CONFLICT 177 177 D -> N (IN REF. 2).  
SO SEQUENCE 266 AA; 30546 MW; 3A7AB59AB986853B CRC64;

Query Match 90.1%; Score 64; DB 1; Length 266;  
Best Local Similarity 83.3%; Pred. No. 0.00061;  
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CMYGVTLHEGN 12  
|||||:|||||

DB 137 CMYGVTLHEGN 148

RESULT 2  
ETC2\_STAUB STANDARD; PRT; 266 AA.

AC P34071;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE ENTEROTOXIN TYPE C-2 PRECURSOR (SEC2).  
GN ENT2.  
OS Staphylococcus aureus.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
OC Bacillus/Staphylococcus group; Staphylococcus.  
OX NCBI\_TaxID=1280;  
[1]  
RP SEQUENCE FROM N.A. AND SEQUENCE OF 28-66.  
RX MEDLINE=69277549; PubMed=2543637;  
RA Bohach G.A., Schlievert P.M.;  
RT "Conservation of the biologically active portions of staphylococcal enterotoxins C1 and C2."  
RL Infect. Immun. 57:2249-2252(1989).  
RN [2]  
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
RX MEDLINE=96027099; PubMed=7582894;  
RA Papageorgiou A.C., Acharya K.R., Shapiro R., Passalacqua E.F.,  
Brehm R.D., Tranter H.S.;  
RT "Crystal structure of the superantigen enterotoxin C2 from Staphylococcus aureus reveals a zinc-binding site."  
RL Structure 3:769-779(1995).  
RN [3]  
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).  
RX MEDLINE=96022987; PubMed=7552730;  
RA Swaminathan S., Furey W.F. Jr., Pletcher J., Sax M.;  
RT "Residues defining V beta specificity in staphylococcal enterotoxins."  
RL Nat. Struct. Biol. 2:680-686(1995).  
RN [4]  
RP COMPARISON OF STRUCTURE OF SEA AND SEC2.  
RX MEDLINE=97334373; PubMed=9191070;  
RA Schad E.M., Papageorgiou A.C., Svensson L.A., Acharya K.R.;  
RT "A structural and functional comparison of staphylococcal enterotoxins A and C2 reveals remarkable similarity and dissimilarity."  
RL J. Mol. Biol. 269:270-280(1997).  
CC -I- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION STAPHYLOCOCCAL FOOD POISONING SYNDROME.  
CC -I- SIMILARITY: THE DIFFERENT S.AUREUS ENTEROTOXINS AND S.PYOGENES PROGENIC EXOTOXINS ARE ALL RELATED.  
DR PIR; A60114; A60114.  
DR PDB; 1STE; 23-DEC-96.  
DR PDB; 1SE2; 08-MAR-96.  
DR InterPro: IPR001961; Staph.Strep.toxin.  
DR Pfam: PF01123; Staph.Strep.toxin.1.  
DR PRINTS; PR00279; BACTRTOXIN.  
DR PROSITE; PS00277; STAPH\_STREP\_TOXIN\_1; 1.  
DR PROSITE; PS00278; STAPH\_STREP\_TOXIN\_2; 1.  
KW Enterotoxin; Toxin; Signal; Superantigen; Zinc; 3D-structure.  
FT CHAIN 1 27  
FT SIGNAL 1 27  
FT CHAIN 28 266 ENTEROTOXIN TYPE C-2.  
FT DISULFID 120 137  
FT METAL 36 36 ZINC.  
FT METAL 110 110 ZINC.  
FT METAL 145 145 ZINC.  
FT METAL 149 149 ZINC.  
SQ SEQUENCE 266 AA; 30604 MW; 8407FB18536FAC08 CRC64;

Query Match 90.1%; Score 64; DB 1; Length 266;  
Best Local Similarity 83.3%; Pred. No. 0.00061;  
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CMYGVTLHEGN 12  
|||||:|||||

DB 137 CMYGVTLHEGN 148

RESULT 3  
ETC3\_STAUB STANDARD; PRT; 266 AA.

AC P23313;  
DT 01-NOV-1991 (Rel. 20, Created)  
DT 01-NOV-1991 (Rel. 20, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE ENTEROTOXIN TYPE C-3 PRECURSOR (SEC3).  
GN ENT3.  
OS Staphylococcus aureus.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
OC Bacillus/Staphylococcus group; Staphylococcus.  
OX NCBI\_TaxID=1280;  
[1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90220508; PubMed=2325627;  
RA Hovde C.J., Hackett S.P., Bohach G.A.;  
RT "Nucleotide sequence of the staphylococcal enterotoxin C3 gene: sequence comparison of all three type C staphylococcal enterotoxins."  
RL Mol. Gen. Genet. 220:329-333(1990).  
RN [2]  
RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS) OF COMPLEX WITH T-CELL RECP.  
RX MEDLINE=97064178; PubMed=8906797;  
RA Fields B.A., Malchioldi E.L., Li H., Yern X., Stauffer C.V.,  
Schlievert P.M., Karjalainen K., Mariuzza R.A.;  
RT "Crystal structure of a T-cell receptor beta-chain complexed with a superantigen."  
RL Nature 384:188-192(1996).  
CC -I- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION STAPHYLOCOCCAL FOOD POISONING SYNDROME.  
CC -I- SIMILARITY: THE DIFFERENT S.AUREUS ENTEROTOXINS AND S.PYOGENES PROGENIC EXOTOXINS ARE ALL RELATED.  
CC -I- SIMILARITY: THE DIFFERENT S.AUREUS ENTEROTOXINS AND S.PYOGENES PROGENIC EXOTOXINS ARE ALL RELATED.  
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CC -----  
DR EMBL; X51661; CAA35972.1; -  
DR PIR; S11885; S11885.  
DR PDB; 1JCK; 12-NOV-97.  
DR InterPro: IPR001961; Staph.Strep.toxin.  
DR Pfam; PF01123; Staph.Strep.toxin.1.  
DR PRINTS; PR00279; BACTRTOXIN.  
DR PROSITE; PS00277; STAPH\_STREP\_TOXIN\_1; 1.  
DR PROSITE; PS00278; STAPH\_STREP\_TOXIN\_2; 1.  
KW Enterotoxin; Toxin; Signal; Superantigen; 3D-structure.  
FT CHAIN 1 27  
FT SIGNAL 1 27  
FT CHAIN 28 266 ENTEROTOXIN TYPE C-3.  
FT DISULFID 120 137 BY SIMILARITY.  
FT CHAIN 120 137  
SQ SEQUENCE 266 AA; 30671 MW; 5ED8A32D11FFCA59 CRC64;

Query Match 90.1%; Score 64; DB 1; Length 266;  
Best Local Similarity 83.3%; Pred. No. 0.00061;  
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CMYGVTLHEGN 12



Db 137 CMVGGTIRKHEGN 148

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|||||:|||||
137 CMVGGTIRKHEGN 148

RESULT 4
ETX\STAU STANDARD; PRT; 257 AA.
ID ETX\STAU STANDARD; PRT; 257 AA.
AC P13163:
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ENTEROTOXIN TYPE A PRECURSOR (SEA).
GN ENTA.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PR1337;
RX MEDLINE=88086892; PubMed=3335483;
RA Beutley M.J., Mekalanos J.J.;
RT "Nucleotide sequence of the type A staphylococcal enterotoxin gene.";
RL J. Bacteriol. 170:34-41(1988).
RN [2]
RP SEQUENCE OF 25-257.
RX MEDLINE=87222293; PubMed=3584106;
RA Huang I.-Y., Hughes J.L., Bergdoll M.S., Schantz E.J.;
RT "Complete amino acid sequence of staphylococcal enterotoxin A.";
RL J. Biol. Chem. 262:7006-7013(1987).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=95354648; PubMed=7628431;
RA Sched E.M., Zaitseva T., Zaitsev V.N., Dohlsten M., Kalland T.,
RT "Crystal structure of the superantigen staphylococcal enterotoxin
RT type A.";
RL EMBO J. 14:3292-3301(1995).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
RX MEDLINE=97113025; PubMed=8943278;
RA Sundstrome M., Hallen D., Svensson A., Sched E., Dohlsten M.,
RT "The Co-crystal structure of staphylococcal enterotoxin type A with
RT Zn2+ at 2.7-A resolution. Implications for major histocompatibility
RT complex class II binding.";
RL J. Biol. Chem. 271:3212-3221(1996).
RN [5]
RP 3D-STRUCTURE MODELING.
RX MEDLINE=96022987; PubMed=7552730;
RA Swaminathan S., Furey W.F. Jr., Pletcher J., Sax M.;
RT "Residues defining V beta specificity in staphylococcal
RT enterotoxins.";
RL Nat. Struct. Biol. 2:680-686(1995).
RN [6]
RP COMPARISON OF STRUCTURE OF SEA AND SEC2.
RX MEDLINE=97334373; PubMed=9191070;
RA Sched E.M., Papageorgiou A.C., Svensson L.A., Acharya K.R.;
RT "A structural and functional comparison of staphylococcal
RT enterotoxins A and C2 reveals remarkable similarity and
RT dissimilarity.";
RL J. Mol. Biol. 269:270-280(1997).
RN [7]
RP SUBUNIT: MONOMER.
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- MISCELLANEOUS: THIS TOXIN SEEMS TO BE CODED BY A BACTERIOPHAGE.
CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
CC PYROGENIC EXOTOXINS ARE ALL RELATED.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M18970; AAA26681.1; -.
DR PIR: A28664; A28664.
DR PIR: A29566; A29566.
DR PDB: 1ESF; 11-JUL-96.
DR PDB: 1SEA; 15-OCT-95.
DR PDB: 1SXT; 19-NOV-97.
DR InterPro: IPR001961; Staph_Strep_toxin.
DR Pfam: PF01123; Staph_Strep_toxin; 1.
DR PRINTS: PR00279; BACTERIOTOXIN.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
KW Enterotoxin; Toxin; Signal; Superantigen; Zinc; 3D-structure.
FT CHAIN 1 24 ENTEROTOXIN TYPE A.
FT DISULFID 120 130
FT METAL 25 25 ZINC.
FT METAL 211 211 ZINC.
FT METAL 249 249 ZINC.
FT METAL 251 251 ZINC.
FT CONFLICT 242 242 T -> S (IN REF. 2).
FT SEQUENCE 257 AA; 29669 MW; ADEBF5BCA1F14677 CRC64;

Query Match 87.38; Score 62; DB 1; Length 257;
Best Local Similarity 83.38; Pred. No. 0.0013;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CMVGGTIRKHEGN 12
Db 130 CMVGGTIRKHEGN 141

RESULT 5
ETX\STAU STANDARD; PRT; 257 AA.
ID ETX\STAU STANDARD; PRT; 257 AA.
AC P12993;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ENTEROTOXIN TYPE E PRECURSOR (SEE).
GN ENTE.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A. AND SEQUENCE OF 28-74.
RC STRAIN=MJB265;
RX MEDLINE=88257005; PubMed=3384800;
RA Couch J.L., Solits M.T., Beutley M.J.;
RT "Cloning and nucleotide sequence of the type E staphylococcal
RT enterotoxin gene.";
RL J. Bacteriol. 170:2954-2960(1988).
RN [2]
RP 3D-STRUCTURE MODELING.
RX MEDLINE=96022987; PubMed=7552730;
RA Swaminathan S., Furey W.F. Jr., Pletcher J., Sax M.;
RT "Residues defining V beta specificity in staphylococcal
RT enterotoxins.";
RL Nat. Struct. Biol. 2:680-686(1995).
RN [3]
RP DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- MISCELLANEOUS: THIS TOXIN SEEMS TO BE CODED BY A BACTERIOPHAGE.
CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
CC PYROGENIC EXOTOXINS ARE ALL RELATED.
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CC or send an email to license@isb-sib.ch).
CC -----
CC DR EMBL; M21319; AAA26617.1; -.
CC DR PIR; A28179; A28179.
CC DR PDB; 1SEE; 15-OCT-95.
CC DR InterPro; IPR001961; Staph.Strep.toxin.
CC DR Pfam; PF01123; Staph.Strep.toxin; 1.
CC DR PRINTS; PR00279; BACTRLOXIN.
CC DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
CC DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
CC KM Enterotoxin; Toxin; Signal; Superantigen; 3D-structure.
CC FT SIGNAL 1 27
CC FT CHAIN 28 257 ENTEROTOXIN TYPE E.
CC SQ SEQUENCE 257 AA; 29358 MW; 27EDA94B97770CE3 CMC64;
OY 1 CMYGVTHN 12
Db 130 CMYGVTHDNN 141
RESULT 6
SPEA_STRPY STANDARD; PRI; 251 AA.
AC P08095;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE EKOTOXIN TYPE A PRECURSOR (SCARLET FEVER TOXIN) (ERYTHROGENIC TOXIN)
DE (SPE A).
OS SPEA.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
OX [1]
RP SEQUENCE FROM N.A.
RP MEDLINE=86166804; PubMed=3514452;
RA Weeks C.R., Ferretti J.J.,
RA "Nucleotide sequence of the type A streptococcal exotoxin
RA (erythrogenic toxin) gene from Streptococcus pyogenes bacteriophage
RA t12.".
RA Infect. Immun. 52:144-150(1986).
RA [2]
RP SEQUENCE FROM N.A.
RP MEDLINE=86284313; PubMed=3526093;
RA Johnson L.P., L'Italien J.J., Schlievert P.M.;
RA "Streptococcal pyrogenic exotoxin type A (scarlet fever toxin) is
RA related to Staphylococcus aureus enterotoxin B.".
RA Mol. Gen. Genet. 203:354-356(1986).
RA [3]
RP X-RAY CRYSTALLOGRAPHY (2.57 ANGSTROMS).
RP MEDLINE=99094887; PubMed=9878045;
RA Papageorgiou A.C., Collins C.M., Gutman D.M., Kline J.B.,
RA O'Brien S.M., Tranter H.S., Acharya K.R.;
RA "Structural basis for the recognition of superantigen streptococcal
RA pyrogenic exotoxin A (SpeA) by MHC class II molecules and T-cell
RA receptors.".
RA EMBO J. 18:9-21(1999).
CC -!- DISEASE: THE STREPTOCOCCAL PYROGENIC TOXINS A, B, AND C ARE
CC THE CAUSATIVE AGENTS OF THE SYMPTOMS ASSOCIATED WITH SCARLET
CC FEVER, HAVE BEEN ASSOCIATED WITH STREPTOCOCCAL TOXIC SHOCK-LIKE
CC DISEASE AND MAY PLAY A ROLE IN THE EARLY EVENTS OF RHEUMATIC
CC FEVER.
CC -!- MISCELLANEOUS: THIS TOXIN SEEMS TO BE CODED BY BACTERIOPHAGE T12.
CC -!- SIMILARITY: THE DIFFERENT S.AUREUS ENTEROTOXINS AND S.PYOGENES
CC PYROGENIC EKOTOXINS ARE ALL RELATED.

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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).
DR	EMBL; U04053; AAC4866.1; -;
DR	EMBL; X03929; CA27568.1; -;
DR	PIR; A26152; A26152.
DR	PIR; S29659; S29659.
PDB	1BIJ; 24-NOV-99.
DR	InterPro: IPR001961; Staph.Strep.toxin.
DR	pfam; PF01123; Staph_Strep_toxin; 1.
DR	PRINTS; PR00279; BACTRLTOXIN.
DR	PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR	PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW	Toxin; Signal; 3D-structure.
FT	SIGNAL
FT	CHAIN 1 30 EXOTOXIN TYPE A.
FT	DISEUFD 117 128
FT	CONFLICT 6 6 K -> E (IN REF. 2).
FT	CONFLICT 17 18 VT -> MK (IN REF. 2).
FT	CONFLICT 25 35 SOEYFAOODP -> LPRGICSTRPK (IN REF. 2).
FT	CONFLICT 40 40 H -> Q (IN REF. 2).
FT	CONFLICT 43 43 S -> N (IN REF. 2).
FT	CONFLICT 47 59 NLQNTVFLGEDP -> TFKIYIFMAYTL (IN REF. 2).
FT	CONFLICT 129 129 I -> L (IN REF. 2).
FT	CONFLICT 165 178 TNKMVTVAQELDVK -> QLRNGNCSRIYST (IN REF. 2).
SQ	SEQUENCE 251 AA; 29246 MW; 54001FEACCCBFCC3 CRC64;
OY	1 CMYGCVTLHEGN 12
Db	128 CIIYGVTHNEGN 139
RESULT 7	I :
ETXB_STAUV	ETXB_STAUV STANDARD; PRT; 266 AA.
AC	P01552;
DT	21-JUL-1986 (Rel. 01, Created)
DT	13-AUG-1987 (Rel. 05, Last sequence update)
DT	15-JUL-1999 (Rel. 38, Last annotation update)
DE	ENTEROTOXIN TYPE B PRECURSOR (SEB).
GN	ENTB.
OS	Staphylococcus aureus.
OC	Bacteria; Firmicutes; Bacillus/Clostridium group;
OC	Bacilli/Staphylococcus group; Staphylococcus.
OX	NCBI_TaxID=1280;
RN	[1]
RX	SEQUENCE FROM N.A.
RX	MEDLINE=86168029; PubMed=3957869;
RA	Jones C.L., Khan S.A.;
RT	"Nucleotide sequence of the enterotoxin B gene from Staphylococcus
RT	aureus ";
RL	J. Bacteriol. 166:29-33(1986).
RN	[2]
RP	SEQUENCE OF 40-91 FROM N.A.
RX	MEDLINE=85298255; PubMed=3898073;
RA	Ranelli D.M., Jones C.L., Johns M.B., Mussey G.J., Khan S.A.;
RT	"Molecular cloning of staphylococcal enterotoxin B gene in
RT	Escherichia coli and Staphylococcus aureus ";
RL	Proc. Natl. Acad. Sci. U.S.A. 82:5850-5854(1985).
RN	[3]

RP SEQUENCE OF 28-266 (S-6).  
 RX MEDLINE=71007902; PubMed=5470821;  
 RA Huang I.-Y., Bergdoll M.S.;  
 RT "The primary structure of staphylococcal enterotoxin B. 3. The  
 RT cyanogen bromide peptides of reduced and aminoethylated enterotoxin  
 RT B, and the complete amino acid sequence.";  
 RL J. Biol. Chem. 245:3518-3525(1970).  
 RN [4]  
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).  
 RX MEDLINE=93063291; PubMed=1436058;  
 RA Swamidathan S., Furey W.F. Jr., Pletcher J., Sax M.;  
 RT "Crystal structure of staphylococcal enterotoxin B, a superantigen.";  
 RL Nature 359:801-806(1992).  
 RN [5]  
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF COMPLEX WITH MHC II.  
 RX MEDLINE=94203282; PubMed=8152483;  
 RA Jardelezky T.S., Brown J.H., Gorga J.C., Stern L.J., Urban R.G.,  
 RA Chl Y.I., Stauffer C., Strominger J.L., Wiley D.C.;  
 RT "Three-dimensional structure of a human class II histocompatibility  
 RT molecule complexed with superantigen.";  
 RL Nature 368:711-718(1994).  
 RN [6]  
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF COMPLEX WITH TCR.  
 RX MEDLINE=99096298; PubMed=9881971;  
 RA Li H., Lierra A., Tsuchiya D., Leder L., Ysern X., Schlievert P.M.,  
 RA Karjalainen K., Mariuzza R.A.;  
 RT "Three-dimensional structure of the complex between a T cell receptor  
 RT beta chain and the superantigen staphylococcal enterotoxin B.";  
 RL Immunity 9:807-816(1998).  
 RN [7]  
 RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).  
 RX MEDLINE=98181012; PubMed=9514739;  
 RA Papageorgiou A.C., Tranter H.S., Acharya K.R.;  
 RT "Crystal structure of microbial superantigen staphylococcal  
 RT enterotoxin B at 1.5-A resolution: implications for superantigen  
 RT recognition by MHC class II molecules and T-cell receptors.";  
 RL J. Mol. Biol. 277:61-79(1998).  
 CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION  
 CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.  
 CC -1- SIMILARITY: THE DIFFERENT S.AUREUS ENTEROTOXINS AND S.PYOGENES  
 CC PROGENIC EXOTOXINS ARE ALL RELATED.  
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 CC -----  
 CC EMBL: M1118; AAA86550.1; -.  
 DR PIR: A01815; ENSAB6.  
 DR PIR: S27360; S27360.  
 DR PDB: 1SEB; 20-JUN-96.  
 DR PDB: 2SEB; 28-JAN-98.  
 DR PDB: 3SEB; 27-MAY-98.  
 DR PDB: 1SE3; 16-JUN-97.  
 DR PDB: 1SE4; 15-OCT-97.  
 DR PDB: 1SBB; 04-MAR-99.  
 DR InterPro: IPR001961; Staph\_Strep\_toxin.  
 DR Pfam: PF01123; Staph\_Strep\_toxin; 1.  
 DR PRINTS: PR00279; BACTRTOXIN.  
 DR PROSITE: PS00277; STAPH\_STREP\_TOXIN\_1; 1.  
 DR PROSITE: PS00278; STAPH\_STREP\_TOXIN\_2; 1.  
 KW Enterotoxin; Toxin; Signal; Superantigen; 3D-structure.  
 FT SIGNAL 1 27  
 FT CHAIN 28 266 ENTEROTOXIN TYPE B.  
 FT DISULFID 120 140  
 FT CONFLICT 36 58  
 FT CONFLICT 69 77 DON -> NND (IN REF. 3).  
 FT CONFLICT 118 118 DOFLYDLI -> NEFDLYL (IN REF. 3).  
 FT CONFLICT 128 130 MISSING (IN REF. 3).  
 FT CONFLICT 133 135 DIN -> NID (IN REF. 3).  
 FT CONFLICT 133 135 OTD -> ENT (IN REF. 3).

FT CONFLICT 149 150 NG -> GN (IN REF. 3).  
 FT CONFLICT 156 156 Y -> YY (IN REF. 3).  
 FT CONFLICT 185 186 OE -> EO (IN REF. 3).  
 FT CONFLICT 233 233 D -> N (IN REF. 3).  
 FT CONFLICT 246 247 DN -> ND (IN REF. 3).  
 SQ SEQUENCE 266 AA; 31436 MW; B6D417F61CF018B0 CRC64;  
 Query Match 83.1%; Score 59; DB 1; Length 266;  
 Best Local Similarity 83.3%; Pred. No. 0.0044;  
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Oy 1 CMYGVTLHEGN 12  
 ||||| | -||  
 Db 140 CMYGVTEHNGN 151  
 RESULT 8  
 ETXD\_STAUB STANDARD; PRT: 258 AA.  
 ID ETXD\_STAUB  
 AC P20723;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE ENTEROTOXIN TYPE D PRECURSOR (SED).  
 GN ENT.D.  
 OS Staphylococcus aureus.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
 OC Bacillus/Staphylococcus group; Staphylococcus.  
 OX NCBI\_TaxID=1280;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89359112; PubMed=2549000;  
 RA Bayles K.W., Tardolo J.J.;  
 RT "Genetic and molecular analyses of the gene encoding staphylococcal  
 RT enterotoxin D.";  
 RL J. Bacteriol. 171:479-4806(1989).  
 RN [2]  
 RP SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).  
 RC STRAIN=ATCC 23235;  
 RX MEDLINE=97157473; PubMed=9003758;  
 RA Sundstroem M., Abrahamson L., Antonsson P., Melindate K., Mourad W.,  
 RA Dohlsten M.;  
 RT "The crystal structure of staphylococcal enterotoxin type D reveals  
 RT Zn2+-mediated homodimerization.";  
 RL EMBO J. 15:6832-6840(1996).  
 CC -1- SUBUNIT: HOMODIMER; ZINC-DEPENDENT.  
 CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION  
 CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.  
 CC -1- SIMILARITY: THE DIFFERENT S.AUREUS ENTEROTOXINS AND S.PYOGENES  
 CC PROGENIC EXOTOXINS ARE ALL RELATED.  
 CC -----  
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 CC -----  
 CC EMBL: M28521; AAB06195.1; -.  
 DR PIR: A33953; A33953.  
 DR HSSP: P13163; 1SXT.  
 DR InterPro: IPR001961; Staph\_Strep\_toxin.  
 DR Pfam: PF01123; Staph\_Strep\_toxin; 1.  
 DR PRINTS: PR00279; BACTRTOXIN.  
 DR PROSITE: PS00277; STAPH\_STREP\_TOXIN\_1; 1.  
 DR PROSITE: PS00278; STAPH\_STREP\_TOXIN\_2; 1.  
 KW Enterotoxin; Toxin; Signal; Superantigen; Zinc.  
 FT SIGNAL 1 25  
 FT CHAIN 26 258 ENTEROTOXIN TYPE D.  
 FT METAL 212 212 ZINC.  
 FT METAL 250 250 ZINC.

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FT METAL 252 252 ZINC.
FT VARIANT 114 114 P->A (IN STRAIN ATCC 23235).
SQ SEQUENCE 258 AA; 29746 MW; 4E7C6A28D42597ED.CRC64;

Query Match
Best Local Similarity 81.7%; Score 58; DB 1; Length 258;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CMGCVTLHEGN 12
   1 11111 1111
DB 131 CTYGGVTPHEGN 142

RESULT 9
SECA_BACSU STANDARD; PRT; 841 AA.
AC P28366;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PREPROTEIN TRANSLOCASE SECA SUBUNIT.
GN SECA OR Div+.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168 / MARBURG;
RX MEDLINE=91192600; PubMed=1901557;
RA Sadate Y., Takamatsu H., Nakamura K., Yamane K.;
RT "Sequencing reveals similarity of the wild-type div+ gene of Bacillus
   subtilis to the Escherichia coli seca gene."
RL Gene 98:101-105(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX Soldo B., Lazarevic V., Manuel C., Karamata D.;
RL submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 1-364 FROM N.A.
RC STRAIN=ATCC 6057;
RX MEDLINE=91375427; PubMed=1832735;
RA Overhoff B., Klein M., Spies M., Freudl R.;
RT "Identification of a gene fragment which codes for the 364 amino-
   terminal amino acid residues of a SecA homologue from Bacillus
   subtilis: further evidence for the conservation of the protein export
   apparatus in gram-positive and gram-negative bacteria."
RL Mol. Gen. Genet. 228:417-423(1991).
CC -1- FUNCTION: INVOLVED IN PROTEIN EXPORT. INTERACTS WITH THE SECY/SECE
   SUBUNITS. SECA HAS A CENTRAL ROLE IN COUPLING THE HYDROLYSIS OF
   ATP TO THE TRANSFER OF PRE-SECRETORY PERIPLASMIC AND OUTER
   MEMBRANE PROTEINS ACROSS THE MEMBRANE.
CC -1- SUBUNIT: PART OF THE PROKARYOTIC PROTEIN TRANSLOCATION APPARATUS
   WHICH COMPRISE SECA, SECB, SECD, SECE, SECF, SECG AND SECY
   (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC SIDE OF MEMBRANE, AND
   CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE SECA FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: D10279; BAA01122.1;
CC EMBL: U56901; AAC44957.1;
CC EMBL: X62035; CAA43977.1;
CC EMBL: Z99122; CAB15547.1;

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DR PIR: J00647; J00647.
DR PIR: S17771; S17771.
DR Subtilisin; BG10741; seca.
DR InterPro: IPR000185; seca.
DR Pfam: PF01043; SecA_protein; 1.
DR PRINTS: PR00906; SECA.
DR PROSITE: PS01312; SECA; 1.
KW Protein transport; ATP-binding; Membrane; Translocation; Transport;
KM Complete proteome.
FT NP_BIND 100 107 ATP (POTENTIAL).
FT CONFLICT 126 126 V->I (IN REF. 3).
SQ SEQUENCE 841 AA; 95530 MW; 9AAC3630139F5EFF.CRC64;

Query Match
Best Local Similarity 60.6%; Score 43; DB 1; Length 841;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 MYGCVTLHEGN 12
   1 111 1111
DB 86 LMGSVALHDCN 96

RESULT 10
HCEL_ORYLA STANDARD; PRT; 270 AA.
ID HCEL_ORYLA
AC P31580;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE HIGH CHORIOLYTIC ENZYME 1 PRECURSOR (EC 3.4.24.67) (HATCHING ENZYME
   ZINC-PROTEASE HCE 1 SUBUNIT) (CHORIOLYSIN H 1).
GN HCE 23.
OS Oryzias latipes (Medaka fish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
OX NCBI_TaxID=8090;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 71-119 AND 208-223.
RC TISSUE=embryo;
RX MEDLINE=93012471; PubMed=1397682;
RA Yasunasu S., Yamada K., Akasaka K., Mitsuana K., Iuchi I.,
RA Shimada H., Yamagami K.;
RT "Isolation of cDNAs for LCE and HCE, two constituent proteases of the
   hatching enzyme of Oryzias latipes, and concurrent expression of
   their mRNAs during development."
RL Dev. Biol. 153:250-258(1992).
CC -1- FUNCTION: PARTICIPATES IN THE BREAKDOWN OF THE EGG ENVELOPE,
   WHICH IS DERIVED FROM THE EGG EXTRACELLULAR MATRIX, AT THE TIME
   OF HATCHING. THUS ALLOWING THE NEWLY HATCHED FISH TO SWIM FREE.
CC HCE BINDS TIGHTLY TO THE EGG ENVELOPE WHILE IT EXERTS THE
   CHORIOLYTIC SMELLING ACTION.
CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF THE INNER LAYER OF FISH EGG
   ENVELOPE. ALSO HYDROLYSES CASEIN AND SMALL MOLECULE SUBSTRATES
   SUCH AS SUC-LEU-LEU-VAL-TYR-|-MCA.
CC -1- COFACTOR: BINDS ONE ZINC ION.
CC -1- SUBCELLULAR LOCATION: STORED AS PROENZYMES IN THE ZMOGEN
   GRANULES.
CC -1- DEVELOPMENTAL STAGE: PRODUCTION OF THE PROTEIN STARTS IN DAY
   2 TO DAY 3 EMBRYOS AND INCREASES THEREAFTER UNTIL HATCHING.
CC -1- PTM: O-GLYCOSYLATED (PROBABLE).
CC -1- MISCELLANEOUS: IN MEDAKA THE HATCHING ENZYME SYSTEM IS COMPOSED OF
   TWO DISTINCT PROTEASES, THE HIGH CHORIOLYTIC ENZYME (HCE) OF
   WHICH THERE ARE TWO ISOFORMS, AND THE LOW CHORIOLYTIC ENZYME
   (LCE).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A (ZINC
   METALLOPROTEASE); ALSO KNOWN AS THE ASTACIN SUBFAMILY.
CC -----
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CC -----  
DR EMBL: M96170; AAA49438.1; -.  
DR PIR: B48826; B48826.  
DR HSSP: P07584; 1IAD.  
DR MEROPS: M12.007; -.  
DR InterPro: IPR001506; Astacin.  
DR InterPro: IPR000130; Zn\_MTPeptide.  
DR Pfam: PF01400; Astacin.1.  
DR PRINTS: PR00480; ASTACIN.  
DR SMART: SM00235; ZnMC.1.  
DR PROSITE: PS00142; ZINC\_PROTEASE.1.  
KW Hydrolase; Metalloprotease; zinc; Glycoprotein; zymogen; Signal.  
FT SIGNAL 1 20  
FT PROPEP 21 70 ACTIVATION PEPTIDE.  
FT CHAIN 71 270 HIGH CHORIOLYTIC ENZYME 1.  
FT METAL 169 169 ZINC (CATALYTIC) (BY SIMILARITY).  
FT ACT\_SITE 170 170 BY SIMILARITY.  
FT METAL 173 173 ZINC (CATALYTIC) (BY SIMILARITY).  
FT METAL 179 179 ZINC (CATALYTIC) (BY SIMILARITY).  
FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 270 AA; 30392 MW; D85C9729063735A CRC64;  
  
Query Match 59.2%; Score 42; DB 1; Length 270;  
Best Local Similarity 58.3%; Pred. No. 3.8;  
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
  
OY 1 CMYGVTLHEGN 12  
Db 161 CMYSGTIQHELN 172  
||| | : || |  
  
RESULT 11  
HCE2\_ORYLA STANDARD; PRT; 279 AA.  
ID HCE2\_ORYLA  
AC P1381;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 01-JUL-1993 (Rel. 26, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE HIGH CHORIOLYTIC ENZYME 2 PRECURSOR (EC 3.4.24.67) (HATCHING ENZYME  
DE ZINC-PROTEASE HCE 2 SUBUNIT) (CHORIOLYSIN H 2).  
GN HCE 21.  
OS Oryzias latipes (Medaka fish).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;  
OC Belontiiformes; Adiantichthyidae; Oryziinae; Oryzias.  
OX NCBI\_TaxID=8090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Embryo;  
RX MEDLINE=93012471; Pubmed=1397682;  
RA Vesunasu S., Yamada K., Akasaka K., Mitsunaga K., Iuchi I.,  
RA Shimada H., Yamagami K.;  
RT Isolation of cDNAs for LCE and HCE, two constituent proteases of the  
RT hatching enzyme of Oryzias latipes, and concurrent expression of  
RT their mRNAs during development.\*;  
RL Dev. Biol. 153:250-258(1992).  
CC -1- FUNCTION: PARTICIPATES IN THE BREAKDOWN OF THE EGG ENVELOPE,  
CC WHICH IS DERIVED FROM THE EGG EXTRACELLULAR MATRIX, AT THE TIME  
CC OF HATCHING. THUS ALLOWING THE NEWLY HATCHED FISH TO SWIM FREE.  
CC HCE BINDS TIGHTLY TO THE EGG ENVELOPE WHILE IT EXERTS THE  
CC CHORIOLYTIC SMELLING ACTION.  
CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF THE INNER LAYER OF FISH EGG  
CC ENVELOPE. ALSO HYDROLYSES CASEIN AND SMALL MOLECULE SUBSTRATES  
CC SUCH AS SUC-LEU-LEU-TYR-I-MCA.  
CC -1- COFACTOR: BINDS ONE ZINC ION.  
CC -1- SUBCELLULAR LOCATION: STORED AS PROENZYMES IN THE ZYMOGEN  
CC GRANULES.

CC -1- DEVELOPMENTAL STAGE: PRODUCTION OF THE PROTEIN STARTS IN DAY  
CC 2 TO DAY 3 EMBRYOS AND INCREASES THEREAFTER UNTIL HATCHING.  
CC -1- PM: O-GLYCOSYLATED (PROBABLE).  
CC -1- MISCELLANEOUS: IN MEDAKA THE HATCHING ENZYME SYSTEM IS COMPOSED OF  
CC TWO DISTINCT PROTEASES, THE HIGH CHORIOLYTIC ENZYME (HCE), OF  
CC WHICH THERE ARE TWO ISOFORMS, AND THE LOW CHORIOLYTIC ENZYME  
CC (LCE).  
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A (ZINC  
CC METALLOPROTEASE); ALSO KNOWN AS THE ASPACIN SUBFAMILY.  
CC -----  
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CC -----  
DR EMBL: M96171; AAA49439.1; -.  
DR HSSP: P07584; 1IAD.  
DR MEROPS: M12.007; -.  
DR InterPro: IPR001506; Astacin.  
DR InterPro: IPR000130; Zn\_MTPeptide.  
DR Pfam: PF01400; Astacin.1.  
DR PRINTS: PR00480; ASTACIN.  
DR SMART: SM00235; ZnMC.1.  
DR PROSITE: PS00142; ZINC\_PROTEASE.1.  
KW Hydrolase; Metalloprotease; zinc; Glycoprotein; zymogen; Signal.  
FT SIGNAL 1 20  
FT PROPEP 21 79 ACTIVATION PEPTIDE.  
FT CHAIN 80 279 HIGH CHORIOLYTIC ENZYME 2.  
FT METAL 178 178 ZINC (CATALYTIC) (BY SIMILARITY).  
FT ACT\_SITE 179 179 BY SIMILARITY.  
FT METAL 182 182 ZINC (CATALYTIC) (BY SIMILARITY).  
FT METAL 188 188 ZINC (CATALYTIC) (BY SIMILARITY).  
FT CARBOHYD 62 62 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 279 AA; 31490 MW; 00244107A8B018BC CRC64;  
  
Query Match 59.2%; Score 42; DB 1; Length 279;  
Best Local Similarity 58.3%; Pred. No. 3.9;  
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
  
OY 1 CMYGVTLHEGN 12  
Db 170 CMYSGTIQHELN 181  
||| | : || |  
  
RESULT 12  
SECA\_CYACA STANDARD; PRT; 895 AA.  
ID SECA\_CYACA  
AC O1911;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE PREPROTEIN TRANSLOCASE SECA SUBUNIT.  
GN SECA.  
OS Cyanidium caldarium.  
OS Chloroplast.  
OC Eukaryota; Rhodophyta; Bangiophyceae; Porphyridiales; Porphyridiaceae;  
OC Cyanidium.  
OX NCBI\_TaxID=2771;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=RR-1;  
RX MEDLINE=20496959; Pubmed=11040290;  
RA Gloeckner G., Rosenthal A., Valentin K.;  
RT The structure and gene repertoire of an ancient red algal plastid  
RT genome.\*;  
RL J. Mol. Evol. 51:382-390(2000).  
CC -1- FUNCTION: INVOLVED IN PROTEIN EXPORT AND IMPORT. SECA HAS A  
CC CENTRAL ROLE IN COUPLING THE HYDROLYSIS OF ATP TO THE TRANSFER OF  
CC PRE-SECRETORY PROTEINS ACROSS THE MEMBRANE.

CC -1- SUBCELLULAR LOCATION: CHLOROPLAST.  
 CC -1- SIMILARITY: BELONGS TO THE SECA FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL: AF02186; AAB82678.1; -.  
 CC InterPro: IPR000185; SECA.  
 CC Pfam: PF01043; SECA.protein; 1.  
 CC PRINTS: PR00906; SECA.  
 CC PROSITE: PS01312; SECA; 1.  
 CC Protein transport; ATP-binding; Chloroplast; Translocation; Transport.  
 CC NP\_BIND 105 112 ATP (BY SIMILARITY).  
 CC SEQUENCE 895 AA; 103753 MW; DB290CFD201EADBC CRC64;  
 SQ  
 Query Match 59.2%; Score 42; DB 1; Length 895;  
 Best Local Similarity 70.0%; Pred. No. 12;  
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 OY 2 MYGGVTLHEG 11  
 DB 91 MIGGIVLHEG 100  
 RESULT 13  
 FIBB.CHICK STANDARD; PRT; 463 AA.  
 AC 002020:  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE FIBRINOGEN BETA CHAIN PRECURSOR (FRAGMENT).  
 GN FGB.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RX MEDLINE=91182745; PubMed=2009286;  
 RA Weisbach L., Oddoux C., Procyk R., Grieninger G.;  
 RT "The beta chain of chicken fibrinogen contains an atypical thrombin  
 RT cleavage site";  
 RL Biochemistry 30:3290-3294(1991).  
 CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT  
 CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET  
 CC AGGREGATION.  
 CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS  
 CC (ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.  
 CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY  
 CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA  
 CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES  
 CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS  
 CC CONVERTED INTO THE HARD CLOT BY FACTOR XIII WHICH CATALYZES THE  
 CC EPSILON-(GAMMA-GUTAMYL)LYSINE CROSS-LINKING BETWEEN GAMMA CHAINS  
 CC (STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT  
 CC MONOMERS.  
 CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.  
 CC -----  
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CC EMBL: M58514; AAA48770.1; -.  
 CC DR PIR: A38463; A38463.  
 CC DR HSSP: P02675; 1FZB.  
 CC DR InterPro: IPR002181; Fibrinogen\_C.  
 CC Pfam: PF00147; fibrinogen\_C; 1.  
 CC SMART: SM00186; FGB; 1.  
 CC DR PROSITE: PS00514; FIBRIN\_AG\_C\_DOMAIN; 1.  
 CC KW Blood coagulation; Plasma; Platelet; Glycoprotein; Sulfation.  
 CC FT NON\_TER 1 1  
 CC FT PEPTIDE <1 17 FIBRINOPEPTIDE B.  
 CC FT CHAIN 18 463 FIBRINOGEN BETA CHAIN.  
 CC FT MOD\_RES 5 5 SULFATION (BY SIMILARITY).  
 CC FT SITE 17 18 CLEAVAGE (BY THROMBIN: RELEASE  
 CC FT DISULFID 69 69 FIBRINOPEPTIDE B).  
 CC FT DISULFID 80 80 INTERCHAIN (WITH ALPHA) (BY SIMILARITY).  
 CC FT DISULFID 197 197 INTERCHAIN (WITH GAMMA) (BY SIMILARITY).  
 CC FT DISULFID 201 201 INTERCHAIN (WITH ALPHA) (BY SIMILARITY).  
 CC FT DISULFID 205 289 INTERCHAIN (WITH GAMMA) (BY SIMILARITY).  
 CC FT DISULFID 215 244 BY SIMILARITY.  
 CC FT DISULFID 397 410 BY SIMILARITY.  
 CC FT CARBOHYD 367 367 N-LINKED (GLCNAC... ) (POTENTIAL).  
 CC SEQUENCE 463 AA; 52678 MW; 2044CD49BA9EC7B CRC64;  
 SQ  
 Query Match 58.5%; Score 41.5; DB 1; Length 463;  
 Best Local Similarity 66.7%; Pred. No. 7.6;  
 Matches 8; Conservative 2; Mismatches 1; Indels 1; Gaps 1;  
 OY 2 MYGGVTLH-BGN 12  
 DB 328 LYGSGTTHNEGN 339  
 RESULT 14  
 ID ERRL YEAST STANDARD; PRT; 437 AA.  
 AC P42222:  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE ENOLASE RELATED PROTEIN 1 (EC 4.2.1.11).  
 GN ERRL OR YMR323W OR YMR924.15.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
 OX NCBI\_TaxID=4932;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=S288C / AB972;  
 RA Churcher C.N., Louis E.J., Barrell B.G., Rajandream M.A., Walsh S.V.;  
 RL Submitted (NOV-1995) to the EMBL/Genbank/DBJ databases.  
 RN [2]  
 RN SEQUENCE OF 120-437 FROM N.A.  
 RC STRAIN=S288C / YPI;  
 RX MEDLINE=95304851; PubMed=7765338;  
 RA Pryde F.E., Huckle T.C., Louis E.J.;  
 RT "Sequence analysis of the right end of chromosome XV in Saccharomyces  
 RT cerevisiae: an insight into the structural and functional  
 RT significance of sub-telomeric repeat sequences";  
 RL Yeast 11:371-382(1995).  
 CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE  
 CC + H(2)O.  
 CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC -----
CC DR EMBL: Z51441: CA90841.1; -.
CC DR EMBL: U23472: AAC48992.1; -.
CC DR HSSP: P00924: INEL.
CC DR SGD: S0005920: ERRI.
CC DR Interpro: IPR000941: Enolase.
CC DR Pfam: PF00113: enolase; 1.
CC DR PRINTS: PR00148: ENOLASE.
CC DR PRODOM: PD000902: Enolase; 1.
CC DR PROSITE: PS00164: ENOLASE; 1.
CC KM Lyase; Glycolysis; Magnesium.
CC FT ACT SITE 160 160
CC FT METAL 247 247 BY SIMILARITY.
CC FT METAL 296 296 MAGNESIUM (BY SIMILARITY).
CC FT METAL 321 321 MAGNESIUM (BY SIMILARITY).
CC SQ SEQUENCE 437 AA; 47312 MW; 143DEF66FB03D13 CRC64;
CC
CC Query Match 57.7%; Score 41; DB 1; Length 437;
CC Best Local Similarity 50.0%; Pred. No. 8.8;
CC Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
CC
CC Db 424 CTVAGHREHDSN 435
CC
CC RESULT 15
CC NEEL_HUMAN STANDARD: PRT; 810 AA.
CC ID NEEL_HUMAN
CC AC Q92832: Q9Y472:
CC DT 01-NOV-1997 (Rel. 35, Created)
CC DT 20-NOV-2001 (Rel. 40, Last sequence update)
CC DT 20-AUG-2001 (Rel. 40, Last annotation update)
CC DE PROTEIN KINASE C-BINDING PROTEIN NEEL1 PRECURSOR (NEU-LIKE PROTEIN 1)
CC DE (NEU-RELATED PROTEIN 1).
CC GN NEEL1 OR NRPL.
CC OS Homo sapiens (Human).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
CC OX NCBI_TaxID=9606;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC TISSUE=Brain;
CC RX MEDLINE=97131504; PubMed=8975702;
CC RA Matanabe T.K., Katagiri T., Suzuki M., Shimizu F., Fujiwara T.,
CC RA Kenemoto N., Nakamura Y., Hirai Y., Maekawa H., Takahashi E.,
CC RT "Cloning and characterization of two novel human CDNs (NEEL1 and
CC RT NEEL2) encoding proteins with six EGF-like repeats."
CC RL Genomics 38:273-276(1996).
CC RN [2]
CC RP SEQUENCE OF 383-810 FROM N.A.
CC RA Tjing K., Vastardis H., Mulliken J.B., Bertolami C., Wen Z.,
CC RA Young M., Tieu A., Kwong E.;
CC RT "Nei homolog gene expression in craniofacial anomalies."
CC RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
CC CC -1-SUBUNIT: HOMOTRIMER. BINDS TO PGC BETA-1 (BY SIMILARITY).
CC CC -1-SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
CC CC -1-DISEASE: EXPRESSED IN CRANIOFACIAL ANOMALIES.
CC CC -1-SIMILARITY: CONTAINS 1 TSP N-TERMINAL DOMAIN.
CC CC -1-SIMILARITY: CONTAINS 5 WVC DOMAINS.
CC CC -1-SIMILARITY: CONTAINS 6 EGF-LIKE DOMAINS.
CC CC -1-CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRAMESHIFTS
CC CC IN POSITIONS 427 AND 771.
CC
CC -----
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CC CC or send an email to license@lsb-sib.ch).

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CC	EMBL	D83017	BA11680.1	-	EMBL	U57523	AAB06946.1	ALT_FRAME	DR	HSSP	P07204	ZADZ	DR	MIM	602319	-	DR	InterPro	IPR000152	Asx_hydroxyl	DR	InterPro	IPR000561	EGF-like	DR	InterPro	IPR001881	EGF_Ca	DR	InterPro	IPR003129	TSPN	DR	InterPro	IPR001007	VMFC	DR	Pfam	PF00008	EGF	4	DR	Pfam	PF00093	VMC	2	DR	SMART	SM00179	EGF_Ca	2	DR	SMART	SM00001	EGF-like	4	DR	SMART	SM00282	lang	1	DR	SMART	SM00210	TSPN	1	DR	SMART	SM00011	VMC	3	DR	SMART	SM00011	VMC_def	1	DR	PROSITE	PS00010	ASX_HYDROXLT	3	DR	PROSITE	PS00022	EGF_1	1	DR	PROSITE	PS01186	EGF_2	3	DR	PROSITE	PS01187	EGF_Ca	3	DR	PROSITE	PS01208	VMFC	2	KM	Glycoprotein	EGF-like domain	Repeat	Signal	FT	SIGNAL	1	16	FT	CHAIN	17	810	PROTEIN KINASE C-BINDING PROTEIN NELL1	FT	DOMAIN	81	230	TSP N-TERMINAL	FT	DOMAIN	273	331	VMFC 1	FT	DOMAIN	335	390	VMFC 2	FT	DOMAIN	391	433	EGF-LIKE 1	FT	DOMAIN	434	475	EGF-LIKE 2	FT	DOMAIN	476	516	EGF-LIKE 3	FT	DOMAIN	515	547	EGF-LIKE 4	FT	DOMAIN	549	595	EGF-LIKE 5	FT	DOMAIN	596	631	EGF-LIKE 6	FT	DOMAIN	632	687	VMFC 3	FT	DOMAIN	692	750	VMFC 4	FT	DOMAIN	752	807	VMFC 5	FT	DOMAIN	810	850	BY SIMILARITY	FT	DOMAIN	851	896	BY SIMILARITY	FT	DOMAIN	897	943	BY SIMILARITY	FT	DOMAIN	944	990	BY SIMILARITY	FT	DOMAIN	991	1037	BY SIMILARITY	FT	DOMAIN	1038	1084	BY SIMILARITY	FT	DOMAIN	1085	1131	BY SIMILARITY	FT	DOMAIN	1132	1178	BY SIMILARITY	FT	DOMAIN	1179	1225	BY SIMILARITY	FT	DOMAIN	1226	1272	BY SIMILARITY	FT	DOMAIN	1273	1319	BY SIMILARITY	FT	DOMAIN	1320	1366	BY SIMILARITY	FT	DOMAIN	1367	1413	BY SIMILARITY	FT	DOMAIN	1414	1460	BY SIMILARITY	FT	DOMAIN	1461	1507	BY SIMILARITY	FT	DOMAIN	1508	1554	BY SIMILARITY	FT	DOMAIN	1555	1601	BY SIMILARITY	FT	DOMAIN	1602	1648	BY SIMILARITY	FT	DOMAIN	1649	1695	BY SIMILARITY	FT	DOMAIN	1696	1742	BY SIMILARITY	FT	DOMAIN	1743	1789	BY SIMILARITY	FT	DOMAIN	1790	1836	BY SIMILARITY	FT	DOMAIN	1837	1883	BY SIMILARITY	FT	DOMAIN	1884	1930	BY SIMILARITY	FT	DOMAIN	1931	1977	BY SIMILARITY	FT	DOMAIN	1978	2024	BY SIMILARITY	FT	DOMAIN	2025	2071	BY SIMILARITY	FT	DOMAIN	2072	2118	BY SIMILARITY	FT	DOMAIN	2119	2165	BY SIMILARITY	FT	DOMAIN	2166	2212	BY SIMILARITY	FT	DOMAIN	2213	2259	BY SIMILARITY	FT	DOMAIN	2260	2306	BY SIMILARITY	FT	DOMAIN	2307	2353	BY SIMILARITY	FT	DOMAIN	2354	2400	BY SIMILARITY	FT	DOMAIN	2401	2447	BY SIMILARITY	FT	DOMAIN	2448	2494	BY SIMILARITY	FT	DOMAIN	2495	2541	BY SIMILARITY	FT	DOMAIN	2542	2588	BY SIMILARITY	FT	DOMAIN	2589	2635	BY SIMILARITY	FT	DOMAIN	2636	2682	BY SIMILARITY	FT	DOMAIN	2683	2729	BY SIMILARITY	FT	DOMAIN	2730	2776	BY SIMILARITY	FT	DOMAIN	2777	2823	BY SIMILARITY	FT	DOMAIN	2824	2870	BY SIMILARITY	FT	DOMAIN	2871	2917	BY SIMILARITY	FT	DOMAIN	2918	2964	BY SIMILARITY	FT	DOMAIN	2965	3011	BY SIMILARITY	FT	DOMAIN	3012	3058	BY SIMILARITY	FT	DOMAIN	3059	3105	BY SIMILARITY	FT	DOMAIN	3106	3152	BY SIMILARITY	FT	DOMAIN	3153	3200	BY SIMILARITY	FT	DOMAIN	3201	3247	BY SIMILARITY	FT	DOMAIN	3248	3294	BY SIMILARITY	FT	DOMAIN	3295	3341	BY SIMILARITY	FT	DOMAIN	3342	3388	BY SIMILARITY	FT	DOMAIN	3389	3435	BY SIMILARITY	FT	DOMAIN	3436	3482	BY SIMILARITY	FT	DOMAIN	3483	3529	BY SIMILARITY	FT	DOMAIN	3530	3576	BY SIMILARITY	FT	DOMAIN	3577	3623	BY SIMILARITY	FT	DOMAIN	3624	3670	BY SIMILARITY	FT	DOMAIN	3671	3717	BY SIMILARITY	FT	DOMAIN	3718	3764	BY SIMILARITY	FT	DOMAIN	3765	3811	BY SIMILARITY	FT	DOMAIN	3812	3858	BY SIMILARITY	FT	DOMAIN	3859	3905	BY SIMILARITY	FT	DOMAIN	3906	3952	BY SIMILARITY	FT	DOMAIN	3953	3999	BY SIMILARITY	FT	DOMAIN</
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Query Match 56.3%; Score 40; DB 1; Length 810;  
Best Local Similarity 63.6%; Pred. No. 24;  
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CMYGSVTLHEG 11  
I: I I I I I I I I  
Db 335 CIYGRKVLAEG 345

Search completed: January 2, 2002, 20:50:16  
Job time: 211 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 2, 2002, 20:52:02 ; Search time 92.66 Seconds  
(Without alignments)  
18.943 Million cell updates/sec

Title: US-09-335-581A-34  
Perfect score: 71  
Sequence: 1 CMYGGVTLHEGN 12

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: SPREMBL\_17:\*  
2: sp.archaea:\*  
3: sp.bacteria:\*  
4: sp.fungi:\*  
5: sp.human:\*  
6: sp.invertebrate:\*  
7: sp.mammal:\*  
8: sp.mhc:\*  
9: sp.organelle:\*  
10: sp.phage:\*  
11: sp.plant:\*  
12: sp.podent:\*  
13: sp.virus:\*  
14: sp.vertibrate:\*  
15: sp.unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65	90.1	268	2	085217
2	64	90.1	234	2	09R5X4
3	64	90.1	239	2	005157
4	64	90.1	239	2	053678
5	64	90.1	239	2	006531
6	64	90.1	239	2	006532
7	64	90.1	239	2	006533
8	64	90.1	239	2	006534
9	64	90.1	239	2	006535
10	64	90.1	271	2	09F0L6
11	63	88.7	258	2	09EZM4
12	62	87.3	260	2	099SU3
13	61	85.9	136	2	099T49
14	60	84.5	222	2	09S5Z4
15	60	84.5	222	2	09R931
16	60	84.5	236	2	054696
17	60	84.5	236	2	054779
18	60	84.5	236	2	057453
19	60	84.5	236	2	P97163

20	58	81.7	179	2	052075	052075 plasmid p1b
21	52	73.2	260	2	099T46	099T46 staphylococ
22	52	73.2	261	2	09EZM8	09EZM8 staphylococ
23	51	71.8	260	2	054738	054738 streptococ
24	51	71.8	260	2	054971	054971 streptococ
25	51	71.8	260	2	054739	054739 streptococ
26	47	66.2	157	2	099RP7	099RP7 staphylococ
27	44	62.0	225	2	091921	091921 streptococ
28	44	62.0	225	2	099Z21	099Z21 streptococ
29	42	59.2	266	13	013116	013116 oryzae lat
30	41	57.7	335	2	09A5S5	09A5S5 caulobacter
31	41	57.7	347	4	09NML4	09NML4 homo sapien
32	41	57.7	437	3	012007	012007 saccharomyc
33	41	57.7	1266	4	09NMF6	09NMF6 homo sapien
34	41	57.7	1353	4	09B158	09B158 homo sapien
35	40	56.3	241	2	053585	053585 staphylococ
36	40	56.3	258	2	09ZNM2	09ZNM2 staphylococ
37	40	56.3	258	2	09EZM3	09EZM3 staphylococ
38	40	56.3	258	2	085382	085382 staphylococ
39	40	56.3	968	4	09NZC0	09NZC0 homo sapien
40	39	54.9	63	2	09EM93	09EM93 streptomyc
41	39	54.9	156	2	09JWR7	09JWR7 bacillus ha
42	39	54.9	270	2	066049	066049 enterobacte
43	39	54.9	593	2	044039	044039 anaplasma m
44	39	54.9	622	2	09APG5	09APG5 anaplasma m
45	39	54.9	623	2	09APG7	09APG7 anaplasma m

## ALIGNMENTS

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RESULT 1
085217 ID 085217 PRELIMINARY; PRT: 268 AA.
AC 085217;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE ENTEROTOXIN J.
GN SEJ.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
CX NCBI_TaxID=1280;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=KSI1410;
RC Zhang S., Iandolo J.J., Stewart G.C.;
RA "The enterotoxin D plasmid of Staphylococcus aureus encodes a second
RT enterotoxin determinant (sej).";
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF053140; AAC78590.1; -.
DR HSSP; P13163; IESF.
DR InterPro: IPR001961; Staph_Strep_toxin.
DR Pfam: PF01123; Staph_Strep_toxin; I.
DR PRINTS; PR00279; BACTRUTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Plasmid.
SQ
SEQUENCE 268 AA; 31230 MW; ACSF3546060ACE22 CRC64;

Query Match 91.5%; Score 65; DB 2; Length 268;
Best Local Similarity 91.7%; Pred. No. 0.00061;
Matches 11; Conservative 0; Mismatches 1; Indels 0;
Gaps 0;

OY 1 CMYGGVTLHEGN 12
Db 130 CMYGGVTLHEGN 141

RESULT 2
```

Q9R5X4  
ID Q9R5X4 PRELIMINARY; PRT; 234 AA.  
AC Q9R5X4;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE ENTEROTOXIN-PYROGENIC TOXIN.  
OS Staphylococcus.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
OC Bacillus/Staphylococcus group.  
OX NCBI\_TaxID=1279;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94325955; PubMed=8049778;  
RA Van den Bussche R.A., Lyon J.D., Bohach G.A.;  
RL Mol. Phylogenet. Evol. 2:281-292(1993).  
DR HSSP; P34071; 1SE2.  
DR InterPro: IPR001961; Staph\_Strep\_toxin.  
DR Pfam: PF01123; Staph\_Strep\_toxin.  
DR PRINTS: PR00279; BACTRLTOXIN.  
DR PROSITE: PS00277; STAPH\_STREP\_TOXIN\_1; 1.  
DR PROSITE: PS00278; STAPH\_STREP\_TOXIN\_2; 1.  
SQ SEQUENCE 234 AA; 27122 MW; D6A7B45FB9810052 CRC64;

Query Match 90.1%; Score 64; DB 2; Length 234;  
Best Local Similarity 83.3%; Pred. No. 0.00079;  
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGGVTLHEGN 12  
Db 105 CMYGGITKHEGN 116

RESULT 3  
ID 005157 PRELIMINARY; PRT; 239 AA.  
AC 005157;  
DT 01-JUL-1997 (TREMBLrel. 04, Created)  
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE TYPE C ENTEROTOXIN (FRAGMENT).  
OS Staphylococcus intermedius.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
OC Bacillus/Staphylococcus group; Staphylococcus.  
OX NCBI\_TaxID=1285;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=95-011195;  
RA Edwards V.M., Deringer J.R., Callantine S.D., Deobald C.F.,  
RA Berger P.H., Kapur V., Stauffacher C.V., Bohach G.A.;  
RA Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U91526; AAB50248.1; -.  
DR HSSP; P23313; 1JCK.  
DR InterPro: IPR001961; Staph\_Strep\_toxin.  
DR Pfam: PF01123; Staph\_Strep\_toxin.  
DR PRINTS: PR00279; BACTRLTOXIN.  
DR PROSITE: PS00277; STAPH\_STREP\_TOXIN\_1; 1.  
DR PROSITE: PS00278; STAPH\_STREP\_TOXIN\_2; 1.  
FT NON\_TER 1  
SQ SEQUENCE 239 AA; 27536 MW; D6606446DDE4191 CRC64;

Query Match 90.1%; Score 64; DB 2; Length 239;  
Best Local Similarity 83.3%; Pred. No. 0.00081;  
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGGVTLHEGN 12  
Db 110 CMYGGITKHEGN 121

RESULT 4

O53678  
ID O53678 PRELIMINARY; PRT; 239 AA.  
AC O53678;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE ENTEROTOXIN (FRAGMENT).  
OS Staphylococcus aureus.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
OC Bacillus/Staphylococcus group; Staphylococcus.  
OX NCBI\_TaxID=1280;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94011313; PubMed=8406814;  
RA Marr J.C., Lyon J.D., Robertson J.R., Luper M., Bohach G.A.;  
RT "Characterization of novel type C staphylococcal enterotoxins:  
biological and evolutionary implications";  
RL Infect. Immun. 61:4254-4262(1993).  
DR EMBL; L13376; AAA26620.1; -.  
DR HSSP; P34071; 1SE2.  
DR InterPro: IPR001961; Staph\_Strep\_toxin.  
DR Pfam: PF01123; Staph\_Strep\_toxin.  
DR PRINTS: PR00279; BACTRLTOXIN.  
DR PROSITE: PS00277; STAPH\_STREP\_TOXIN\_1; 1.  
DR PROSITE: PS00278; STAPH\_STREP\_TOXIN\_2; 1.  
KW Enterotoxin.  
FT NON\_TER 1  
SQ SEQUENCE 239 AA; 27618 MW; A13E7EB25C6989C2 CRC64;

Query Match 90.1%; Score 64; DB 2; Length 239;  
Best Local Similarity 83.3%; Pred. No. 0.00081;  
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGGVTLHEGN 12  
Db 110 CMYGGITKHEGN 121

RESULT 5  
ID 006531 PRELIMINARY; PRT; 239 AA.  
AC 006531;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE ENTEROTOXIN TYPE C-4 (SEC4446) (FRAGMENT).  
OS Staphylococcus aureus.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
OC Bacillus/Staphylococcus group; Staphylococcus.  
OX NCBI\_TaxID=1280;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=4446;  
RX MEDLINE=94011313; PubMed=8406814;  
RA Marr J.C., Lyon J.D., Robertson J.R., Luper M., Bohach G.A.;  
RT "Characterization of novel type C staphylococcal enterotoxins:  
biological and evolutionary implications";  
RL Infect. Immun. 61:4254-4262(1993).  
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION  
STAPHYLOCOCCAL FOOD POISONING SYNDROME.  
CC -1- SIMILARITY: THE DIFFERENT S. AUEREUS ENTEROTOXINS AND S. PYOGENES  
PYROGENIC EXOTOXINS ARE ALL RELATED.  
CC EMBL; L13374; AAA26618.1; -.  
DR HSSP; P34071; 1SE2.  
DR InterPro: IPR001961; Staph\_Strep\_toxin.  
DR Pfam: PF01123; Staph\_Strep\_toxin.  
DR PRINTS: PR00279; BACTRLTOXIN.  
DR PROSITE: PS00277; STAPH\_STREP\_TOXIN\_1; 1.  
DR PROSITE: PS00278; STAPH\_STREP\_TOXIN\_2; 1.  
KW Enterotoxin; Toxin; Supranatigen.  
FT NON\_TER 1  
SQ SEQUENCE 239 AA; 27612 MW; BB7BD6204731ED24 CRC64;

Query Match 90.1%; Score 64; DB 2; Length 239;  
Best Local Similarity 83.3%; Pred. No. 0.00081;  
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CMYGVTLHEGN 12  
|||||:|||||  
Db 110 CMYGGITKHEGN 121

RESULT 6  
ID 006532 PRELIMINARY; PRT: 239 AA.  
AC 006533;  
DT 01-NOV-1996 (TREMblrel. 01, Created)  
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
DE ENTEROTOXIN TYPE C-7 (SEC740N) (FRAGMENT).  
OS Staphylococcus aureus.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
OC Bacillus/Staphylococcus group; Staphylococcus.  
OX NCBI\_TaxID=1280;  
RM [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=740N;  
RX MEDLINE=94011313; Pubmed=8406814;  
RA Marr J.C., Lyon J.D., Roberson J.R., Lupher M., Bohach G.A.;  
RT "Characterization of novel type C staphylococcal enterotoxins:  
biological and evolutionary implications."  
RL Infect. Immun. 61:4254-4262(1993).  
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION  
STAPHYLOCOCCAL FOOD POISONING SYNDROME.  
CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES  
PYROGENIC EXOTOXINS ARE ALL RELATED.  
DE EMBL: L13375; AAA26619.1; -  
DR HSSP: P34071; 1SE2.  
DR InterPro: IPR001961; Staph\_Strep\_toxin.  
DR Pfam: PF01123; Staph\_Strep\_toxin; 1.  
DR PRINTS: PR00279; BACTRLTOXIN.  
DR PROSITE: PS00277; STAPH\_STREP\_TOXIN\_1; 1.  
DR PROSITE: PS00278; STAPH\_STREP\_TOXIN\_2; 1.  
KM Enterotoxin; Toxin; Superantigen.  
FT NON\_TER 1  
SQ SEQUENCE 239 AA; 27642 MW; C77009F46BC8D645 CRC64;

Query Match 90.1%; Score 64; DB 2; Length 239;  
Best Local Similarity 83.3%; Pred. No. 0.00081;  
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CMYGVTLHEGN 12  
|||||:|||||  
Db 110 CMYGGITKHEGN 121

RESULT 7  
ID 006533 PRELIMINARY; PRT: 239 AA.  
AC 006533;  
DT 01-NOV-1996 (TREMblrel. 01, Created)  
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
DE ENTEROTOXIN TYPE C (SECCOPELAND) (FRAGMENT).  
OS Staphylococcus aureus.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
OC Bacillus/Staphylococcus group; Staphylococcus.  
OX NCBI\_TaxID=1280;  
RM [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MNCOPELAND;  
RX MEDLINE=94011313; Pubmed=8406814;  
RA Marr J.C., Lyon J.D., Roberson J.R., Lupher M., Bohach G.A.;

RT "Characterization of novel type C staphylococcal enterotoxins:  
biological and evolutionary implications."  
RL Infect. Immun. 61:4254-4262(1993).  
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION  
STAPHYLOCOCCAL FOOD POISONING SYNDROME.  
CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES  
PYROGENIC EXOTOXINS ARE ALL RELATED.  
DE EMBL: L13378; AAA26622.1; -  
DR HSSP: P34071; 1STE.  
DR InterPro: IPR001961; Staph\_Strep\_toxin.  
DR Pfam: PF01123; Staph\_Strep\_toxin; 1.  
DR PRINTS: PR00279; BACTRLTOXIN.  
DR PROSITE: PS00277; STAPH\_STREP\_TOXIN\_1; 1.  
DR PROSITE: PS00278; STAPH\_STREP\_TOXIN\_2; 1.  
KM Enterotoxin; Toxin; Superantigen.  
FT NON\_TER 1  
SQ SEQUENCE 239 AA; 27651 MW; A21A954386AE8625 CRC64;

Query Match 90.1%; Score 64; DB 2; Length 239;  
Best Local Similarity 83.3%; Pred. No. 0.00081;  
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CMYGVTLHEGN 12  
|||||:|||||  
Db 110 CMYGGITKHEGN 121

RESULT 8  
ID 006534 PRELIMINARY; PRT: 239 AA.  
AC 006534;  
DT 01-NOV-1996 (TREMblrel. 01, Created)  
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
DE ENTEROTOXIN TYPE C (SECOVINE) (FRAGMENT).  
OS Staphylococcus aureus.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
OC Bacillus/Staphylococcus group; Staphylococcus.  
OX NCBI\_TaxID=1280;  
RM [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94011313; Pubmed=8406814;  
RA Marr J.C., Lyon J.D., Roberson J.R., Lupher M., Bohach G.A.;  
RT "Characterization of novel type C staphylococcal enterotoxins:  
biological and evolutionary implications."  
RL Infect. Immun. 61:4254-4262(1993).  
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION  
STAPHYLOCOCCAL FOOD POISONING SYNDROME.  
CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES  
PYROGENIC EXOTOXINS ARE ALL RELATED.  
DE EMBL: L13379; AAA26623.1; -  
DR HSSP: P34071; 1SE2.  
DR InterPro: IPR001961; Staph\_Strep\_toxin.  
DR Pfam: PF01123; Staph\_Strep\_toxin; 1.  
DR PRINTS: PR00279; BACTRLTOXIN.  
DR PROSITE: PS00277; STAPH\_STREP\_TOXIN\_1; 1.  
DR PROSITE: PS00278; STAPH\_STREP\_TOXIN\_2; 1.  
KM Enterotoxin; Toxin; Superantigen.  
FT NON\_TER 1  
SQ SEQUENCE 239 AA; 27517 MW; F354742619C8D196 CRC64;

Query Match 90.1%; Score 64; DB 2; Length 239;  
Best Local Similarity 83.3%; Pred. No. 0.00081;  
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CMYGVTLHEGN 12  
|||||:|||||  
Db 110 CMYGGITKHEGN 121

RESULT 9

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006535 ID 006535 PRELIMINARY; PRT; 239 AA.
AC 006535;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE ENTEROTOXIN TYPE C-3 (SEC3) (FRAGMENT).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-FRI 909;
RX MEDLINE=94011313; PubMed=8406814;
RX Marr J.C., Lyon J.D., Roberson J.R., Luppner M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
RT biological and evolutionary implications."
RL Infect. Immun. 61:4234-4262(1993).
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
CC PYROGENIC EXOTOXINS ARE ALL RELATED.
EMBL: L33377; AAA26621.1; -.
DR HSSP; P23313; 1JCK.
DR InterPro; IPR001961; Staph_Strep_toxin.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Enterotoxin; Toxin; Superantigen.
FT NON_TER 1
SQ SEQUENCE 239 AA; 27648 MW; CC3CB3B04E4119E0 CRC64;

Query Match 90.1%; Score 64; DB 2; Length 239;
Best Local Similarity 83.3%; Pred. No. 0.00081;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CMYGVTLHEGN 12
DB 110 CMYGVTLHEGN 121

RESULT 10
Q9F0L6 PRELIMINARY; PRT; 271 AA.
AC 09F0L6;
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DE STAPHYLOCOCCAL ENTEROTOXIN C-BOVINE.
GN SEC-BOV.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2056668; PubMed=11114901;
RX Fitzgerald J.R., Monday S.R., Foster T.J., Bohach G.A., Hartigan P.J.,
RX Meaney W.J., Smyth C.J.;
RT "Characterization of a putative pathogenicity island from bovine
RT Staphylococcus aureus encoding multiple superantigens."
RL J. Bacteriol. 183:63-70(2001).
EMBL: AF217235; AAG29599.1; -.
DR InterPro; IPR001961; Staph_Strep_toxin.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
SQ SEQUENCE 271 AA; 3493F6228B042F10 CRC64;

Query Match 90.1%; Score 64; DB 2; Length 271;

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Best Local Similarity 83.3%; Pred. No. 0.00094;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CMYGVTLHEGN 12
DB 142 CMYGVTLHEGN 153

RESULT 11
Q9EZM4 PRELIMINARY; PRT; 258 AA.
AC 09EZM4;
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE SEK (ENTEROTOXIN SEN).
GN SEK OR SEN OR SAI643.
OS Staphylococcus aureus, and
OS Staphylococcus aureus subsp. aureus N315.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
OX NCBI_TaxID=1280, 158879;
RN [1]
RP SEQUENCE FROM N.A.
RX SPECIES=S.aureus; STRAIN=A900322;
RX MEDLINE=20571956; PubMed=11123352;
RX Jarraud S., Peyrat M.A., Lim A., Tristan A., Bes M., Mougel C.,
RX Etienne J., Vandenesch F., Bonneville M., Lina G.;
RT "egc, A highly prevalent operon of enterotoxin gene, forms a putative
RT nursery of superantigens in Staphylococcus aureus."
RT J. Immunol. 166:669-677(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX SPECIES=S.aureus subsp. aureus N315;
RX Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RX Cui L., Oguchi A., Aoki K.I., Nagai Y., Ito T., Kanamori M.,
RX Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y.,
RX Takahashi N.K., Sawano T., Inoue R.I., Kaito C., Sekimizu K.,
RX Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M.,
RX Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M.,
RX Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RL Lancet 357:1225-1240(2001).
EMBL: AF285760; AAG36956.1; -.
DR EMBL; AP003135; BAB42911.1; -.
DR InterPro; IPR001961; Staph_Strep_toxin.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
KW Complete proteome.
SQ SEQUENCE 258 AA; 29676 MW; 8A6C074F3E1F82D2 CRC64;

Query Match 88.7%; Score 63; DB 2; Length 258;
Best Local Similarity 75.0%; Pred. No. 0.0013;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CMYGVTLHEGN 12
DB 133 CMYGVTLHEGN 144

RESULT 12
Q99SU3 PRELIMINARY; PRT; 260 AA.
AC 099SU3;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE ENTEROTOXIN P.
GN SEP OR SAI761.
OS Staphylococcus aureus subsp. aureus N315.

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OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.I., Nagai Y., Lian J., Ito T., Kanamori M.,
RA Matsunaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y.,
RA Takahashi N.K., Sawano T., Inoue R.I., Kaito C., Sekimizu K.,
RA Hirakawa H., Kunara S., Goto S., Yabuzaki J., Kanehisa M.,
RA Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M.,
RA Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RL Lancet 357:1225-1240(2001).
DR EMBL; AF003135; BAB43036.1; -.
KW Complete proteome.
SQ SEQUENCE 260 AA; 29708 MW; 087C5B4EC028CFDB CRC64;

Query Match 87.3%; Score 62; DB 2; Length 260;
Best Local Similarity 83.3%; Pred. No. 0.0021;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CMYGVTLHEGN 12
Db 133 CMYGVTLHDNN 144

RESULT 13
ID 099749 PRELIMINARY; PRT; 136 AA.
AC 099749:
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE ENTEROTOXIN YENT2.
YENT2 OR SA1644.
OS Staphylococcus aureus subsp. aureus N315.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.I., Nagai Y., Lian J., Ito T., Kanamori M.,
RA Matsunaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y.,
RA Takahashi N.K., Sawano T., Inoue R.I., Kaito C., Sekimizu K.,
RA Hirakawa H., Kunara S., Goto S., Yabuzaki J., Kanehisa M.,
RA Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M.,
RA Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RL Lancet 357:1225-1240(2001).
DR EMBL; AF003135; BAB42912.1; -.
KW Complete proteome.
SQ SEQUENCE 136 AA; 15945 MW; D7CB619820C45FE CRC64;
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Query Match 85.9%; Score 61; DB 2; Length 136;
Best Local Similarity 83.3%; Pred. No. 0.0015;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CMYGVTLHEGN 12
Db 5 CMYGVTEHDGN 16

RESULT 14
ID 09S524 PRELIMINARY; PRT; 222 AA.
AC 09S524:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
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DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE EXOTOXIN TYPE A (FRAGMENT).
GN SPEA.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RA Bessen D.E., Izso M.W., Fiorentino T.R., Carlingal R.M., Beall B.;
RT "Genetic linkage of exotoxin alleles and emm gene markers for tissue
RT tropism in group A streptococci."
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF029051; AAD1315.1; -.
DR HSSP; P08095; 1B12.
DR InterPro; IPR001961; Staph.Strep.-toxin.
DR Pfam; PF01123; Staph.Strep.toxin; 1.
DR PRINTS; PR00279; BACTRTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
FT NON_TER 222
SQ SEQUENCE 222 AA; 25759 MW; 48BB7ADDCD91FBA3 CRC64;

Query Match 84.5%; Score 60; DB 2; Length 222;
Best Local Similarity 83.3%; Pred. No. 0.004;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CMYGVTLHEGN 12
Db 108 CMYGVTLHEGN 119

RESULT 15
ID 09R931 PRELIMINARY; PRT; 222 AA.
AC 09R931:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE EXOTOXIN A (FRAGMENT).
GN SPEA.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RA Bessen D.E., Izso M.W., Fiorentino T.R., Carlingal R.M.,
RA Hollingshead S.R., Beall B.;
RT "Genetic linkage of exotoxin alleles and emm gene markers for tissue
RT tropism in group A streptococci."
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF055698; AAD11624.1; -.
DR HSSP; P08095; 1B12.
DR InterPro; IPR001961; Staph.Strep.-toxin.
DR Pfam; PF01123; Staph.Strep.toxin; 1.
DR PRINTS; PR00279; BACTRTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
FT NON_TER 222
SQ SEQUENCE 222 AA; 25759 MW; 48BB7ADDCD91FBA3 CRC64;
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QY 1 CMGCVTLHEGN 12  
|:|||||  
Db 108 CIXGVTNHEGN 119

Search completed: January 2, 2002, 20:52:02  
Job time: 227 sec